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(54) Title: CHARATERIZATION OF SINGLE NUCLEOTIDE POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES			
(57) Abstract <p>The invention provides nucleic acid segments of the human genome, particularly nucleic acid segments from the coding region of a gene, including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking or containing these sites are also provided. The nucleic acids, primers and probes are used in applications such as phenotype correlations, forensics, paternity testing, medicine and genetic analysis.</p>			

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CHARACTERIZATION OF SINGLE NUCLEOTIDE POLYMORPHISMS
IN CODING REGIONS OF HUMAN GENES

RELATED APPLICATION

This application claims the benefit of U.S. Provisional Application Serial
5 No. 60/127,248, filed March 31, 1999, the entire teachings of which are incorporated
herein by reference.

GOVERNMENT SUPPORT

The invention was supported, in whole or in part, by grant 5-P50-HG00098-
09 SNP from the National Institutes of Health (NCHGR) and grant 1-R01-
10 HL61774-01 from the National Institutes of Health (NHLBI). The Government has
certain rights in the invention.

BACKGROUND OF THE INVENTION

A major goal in human genetics is to understand the role of common genetic
variants in susceptibility to common diseases (N. Risch and K. Merikangas, *Science*,
15 273:1516 (1996.); E. S. Lander, *Science*, 274:536 (1996); F.S. Collins, *et al.*,
Science, 278:1580 (1997)). This requires assembling an extensive catalogue of
single-nucleotide polymorphisms (SNPs) and performing systematic association
studies for particular diseases.

The human population has relatively limited genetic diversity, reflecting its
20 young age and historically small size (F. J. Ayala *et. al.*, *Proc. Natl. Acad. Sci.*,
91:6787 (1994)). Given the restricted nature of the allelic spectrum, some authors
have recently suggested that it should eventually be possible to collect all common
SNPs in the human population and have hypothesized that such common variants
may underlie much of the genetic risk of common disease (N. Risch and K.
25 Merikangas, *Science*, 273:1516 (1996.); E. S. Lander, *Science*, 274:536 (1996); F.S.
Collins, *et al.*, *Science*, 278:1580 (1997)). This is in contrast to the situation for rare

Collins, *et al.*, *Science*, 278:1580 (1997)). This is in contrast to the situation for rare genetic diseases, which are primarily caused by a large number of distinct alleles that are recent, rare and highly penetrant. Important examples of associations to common (>1%) alleles include the ApoE4 allele in Alzheimer's disease, the Factor V^{Leiden} allele in deep-venous thrombosis, and the CCR5-Δ32 in resistance to HIV infection (A. M. Saunders *et al.*, *Neurology*, 43:1467 (1993); R. M. Bertina, *Nature*, 369:64 (1994); M. Dean *et al.*, *Science*, 273:1856 (1996)). The most relevant variants are likely to be those in coding and regulatory regions of genes.

SUMMARY OF THE INVENTION

As described herein, the nature of SNPs in the coding regions of human genes has been explored. SNPs were identified in 106 genes relevant to cardiovascular disease, endocrinology and neuropsychiatry, by screening an average of 114 independent alleles using two independent screening methods. To ensure high accuracy, all reported SNPs were confirmed by DNA sequencing. A total of 545 SNPs were identified, including 395 coding-regions SNPs (cSNPs) divided roughly equally between those causing synonymous and non-synonymous changes. The cSNPs most likely to influence disease, those that alter the amino acid sequence of the encoded protein, show strikingly different properties: they occur at a lower rate and with lower allele frequencies. This likely reflects selection acting against deleterious alleles during human evolution. The lower allele frequency of cSNPs has important implications for the number of chromosomes that must be sampled to construct a comprehensive catalogue of human cSNPs.

The invention relates to a gene which comprises a single nucleotide polymorphism at a specific location. In a particular embodiment the invention relates to the variant allele of a gene having a single nucleotide polymorphism, which variant allele differs from a reference allele by one nucleotide at the site(s) identified in Figures 5A-5Q. Complements of these nucleic acid segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 5-10, 5-15, 10-20, 5-25, 10-30, 10-50 or 10-100 bases long. The invention further relates to gene products encoded by genes and oligonucleotides of the invention.

The invention further provides allele-specific oligonucleotides that hybridize to a gene comprising a single nucleotide polymorphism or to the complement of the gene. These oligonucleotides can be probes or primers.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in Figures 5A-5Q. Optionally, a set of bases occupying a set of the polymorphic sites shown in Figures 5A-5Q is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic site or sites in the individuals tested.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a graph showing minor allele frequency by polymorphism type. The percentage of cSNPs having minor allele frequency classified as low (<5%), medium (5-15%) or high (>15%) frequency is displayed for synonymous, non-synonymous and non-coding SNPs.

Figure 2 is a graph showing the distribution of nucleotide diversity. Normalized frequency of variant sites, θ , was calculated for the coding region of each gene. The graph shows the percentage of genes having θ in the indicated range.

Figures 3A and 3B are a table showing a summary of polymorphisms in 106 human genes described herein. Column 1 shows the name of the gene as used in Online Mendelian Inheritance in Man. Column 2 shows the number of coding base pairs screened. Column 3 shows the number of synonymous (or silent) polymorphisms identified. Column 4 shows the number of non-synonymous polymorphisms identified. Column 5 shows the number of non-coding base pairs screened. Column 6 shows the number of non-coding polymorphisms, including those in introns and untranslated regions (UTR), identified.

Figure 4 is a table showing polymorphism rates for different classes of sites.

Figures 5A-5Q are a table showing the specific polymorphisms identified in the genes studied as described herein. Column 1 shows the laboratory

designation for the polymorphism. Column 2 shows the name of the gene as used in Online Mendelian Inheritance in Man. Column 3 shows the reference nucleotide which occupies the polymorphic site in the reference allele. Column 4 shows the variant nucleotide which occupies the polymorphic site in the variant allele.

- 5 Column 5 shows the reference amino acid encoded by the codon which contains the polymorphic site in the reference allele. Column 6 shows the variant or alternate amino acid encoded by the codon which contains the polymorphic site in the variant allele. Column 7 indicates whether the polymorphism is located in the coding or non-coding region of the gene. Column 8 shows the assay number in which the
- 10 polymorphism was assessed. Columns 9 and 10 show the forward and reverse primers, respectively, which were used to identify the polymorphism. Column 11 shows the sequence of the gene used in the assay, with the polymorphic site indicated by brackets and the primers shown in capital letters. Column 12 shows the total number of nucleotides given in Column 11.

15 DETAILED DESCRIPTION OF THE INVENTION

- There is a rich literature concerning nucleotide variation in model systems, particularly in *Drosophila* (E. N. Moriyama and J. R. Powell., *Mol. Biol. Evol.*, 13:261 (1996)), but sequence variation in human genes has been studied only in limited ways. A small number of studies have focused on individual genes (such as
- 20 beta-globin and lipoprotein lipase) in many individuals, and one study examined 49 genes by comparing two independent sequences deposited in public databases (R. M. Harding *et. al.*, *Am. J. Hum. Genet.*, 60:772 (1997); D. A. Nickerson *et. al.*, *Nature Genetics*, 19:233 (1998); W. H. Li and L.A. Sadler, *Genetics* 129:513 (1991)). To perform a more comprehensive survey, as described herein, a collection
- 25 of 106 genes were selected whose protein products play important roles in the cardiovascular, endocrine and neurological systems (Figures 3A-3B and Figures 5A-5Q). Gene sequences were obtained from the Genbank and TIGR databases. Where multiple sequence depositions were available, a consensus sequence was derived. Determination of coding sequence, untranslated regions and
- 30 intronic regions was based on annotation in the public database, although internal

checks were performed to ensure accurate determination of start and stop codons, open reading frames and the like.

The genes were chosen because of their relevance to common, clinically significant diseases, such as coronary artery disease, diabetes, and schizophrenia.

- 5 They encode proteins involved in coagulation, lipid metabolism, energy metabolism, neuroendocrine physiology, neurotransmission and central nervous system development. Variation in these genes was studied in a sample including Caucasians, African-Americans, African Pygmies and Asians, with an average of 114 chromosomes screened for each gene. Of the samples screened, 30 were from
- 10 Caucasian individuals, 14 from Asian, 10 African American and 7 Africans. The average number of individuals successfully screened for each gene was 57, with the precise number successfully screened varying among genes. Cell lines were obtained from Coriell Cell Repository, and DNA prepared according to standard protocols. In addition, 10 of the Caucasian samples used in this study were obtained
- 15 as anonymous blood samples from the Physician's Health Study (gift of Charles Hennekens and J. Michael Gaziano). The sample size provides greater than 65% power to detect alleles with frequency of 1%.

- Overall, the sample of 114 chromosomes was screened for SNPs in a total of 195.4 kb, consisting of 135.8 kb of coding regions and 59.6 kb from adjacent
- 20 non-coding region (untranslated region (UTR) and introns). Sequences were amplified by the polymerase chain reaction (PCR) and screened by two independent methods. The first method involved hybridization of labeled PCR products to variant detector arrays (VDAs) (that is, high density DNA probe arrays containing oligonucleotides specific for the sequences under study) (M. Chee *et al.*, *Science*, 274:610 (1996); D. G. Wang *et al.*, *Science*, 280:1077 (1998)); variant sequences
- 25 typically give rise to altered hybridization patterns. These chips contained variant detector arrays (VDA) (M. Chee *et al.*, *Science* 274:610 (1996)).

- Using VDAs, candidate SNPs were identified using a combination of three algorithms followed by visual inspection. For each base position and strand queried
- 30 there are four VDA features: one contains the expected base (the reference sequence) in the central position and the other three features contain central substitution bases (in the background of the reference sequence). The base-calling

algorithm looked for positions at which hybridization to a substitution base gives a stronger signal than the reference base. The second algorithm (mutant fraction) examined the reference base and each one of the substitution bases in turn and calculates the fraction of signal present in the non-reference base. The final
5 algorithm (footprint detection) depends upon a loss of signal at the reference positions surrounding a nucleotide substitution. These algorithms are combined to yield a confidence score of "certain" or "likely" for each candidate polymorphism. Two analysts independently scored the data, and candidate polymorphisms found by either observer were included in subsequent confirmation tests. PCR assays
10 spanning each exon were designed using Primer 3.0 release 0.7. PCR was performed according to standard protocols, and assays destined to be hybridized to the same chip design were pooled together. Chip samples were prepared and hybridized as described in D.G. Wang *et al.* (*Science* 280:1077 (1998)), except that pools consisting of about 100 assays contained 5-6 μ g of amplified material. In all,
15 854 assays (average size of 300 bp, covering 106 genes) were amplified from each individual and were hybridized to 12 distinct chip designs. The probe arrays were designed to query only the coding sequence for some genes, while other genes contained the entire mRNA and/or surrounding intron (Figures 3A-3B). The second method involved subjecting PCR products to Denaturing HPLC (dHPLC) (P. J. Oefner and P. A. Underhill, *Am. J. Hum. Genet.*, 57:A266 (1995)) at a critical
20 temperature; heterozygous individuals typically give rise to heteroduplex products with altered denaturation and migration properties.

Sequences were amplified as above except that the final extension in the PCR protocol was followed by denaturation and slow reannealing to allow
25 heteroduplex formation. A total of 6 μ l of each individual PCR product was injected into Wave DNA Fragment Analysis System (Transgenomic). A total of 592 of the VDA assays (covering the 89 genes attempted with this method) were successfully screened by DHPLC. Only assays of >160 base pairs were used for DHPLC, because shorter assays performed unreliably for mutation detection. The
30 DHPLC parameters (percentage of acetonitrile, column temperature) used for each fragment were automatically calculated using a novel predictive algorithm, and DHPLC traces were analyzed using the clustering program ASH v2.0. A scoring

algorithm was developed based upon the similarity score by ASHv2.0 and contour of the elution profile.

Because both screening methods can generate to a significant number of false positives, it was important to confirm every reported SNP. Samples implicated by either method as containing a candidate SNP were thus subjected to fluorescent dideoxy sequencing, either to confirm the presence of the SNP (in the case of the chip) or to identify and confirm the presence of the SNP (in the case of DHPLC). Such confirmation proved essential for eliminating false positives.

Candidate SNPs were either validated (if found by VDAs) or identified (if implicated by DHPLC) by DNA sequencing. For this purpose, sequences were amplified with PCR primers tailed with standard M13 sequencing sites (-21 forward and -28 reverse) and conventional dye-primer sequencing was performed on ABI 377 sequencers. For candidate SNPs discovered by VDAs, one individual was chosen (a candidate homozygous variant, when available, or a candidate heterozygote) and sequencing was performed on one strand to confirm by visual inspection the presence of the SNP at the indicated position. For amplicons found to be polymorphic by DHPLC, two individuals were selected representing each distinct elution pattern observed and were sequenced on both strands to discover the variant base or bases. Sequences were base-called by the Phred program, assembled by the Phrap program, and polymorphism candidates were identified by the PolyPhred program (D. A. Nickerson *et. al.*, *NAR*, 25:2745 (1997)). All results were visually inspected by at least two observers.

The overall false positive rate for VDAs was 45%. The rate was much lower (about 10%) for certain chip designs, synthesis protocols, and for candidate polymorphisms scored as "certain." The false positive rate among fragments displaying an altered elution pattern by DHPLC was similar (40%). The false positive rates reflect the thresholds employed for declaring a candidate SNP, which were chosen to ensure high sensitivity.

A total of 545 SNPs were identified in the 195 kb surveyed, consisting of 150 non-coding SNPs and 395 cSNPs. Results from these studies are shown in the Figures. The complete data are available on the web site http://www.genome.wi.mit.edu/cvar_snps; access to this website can be gained

using the guestname "snp_pilot" and the password "noynek". In the future, access to this website may be available to the public, and thus, no guestname or password may be needed.

To directly determine the false-negative rate of the screen, conventional
 5 DNA sequencing was performed on ten of the genes (THPO, TBAX2R, PTHLH, IGF2, HTR2A, HTR1A, GHR, GABRB1, F10, and CYP11B1) spanning 25.2 kb in twenty individuals. Sequencing was performed on both strands using dye-primer chemistry and sequence traces were interpreted using PolyPhred (D.A. Nickerson *et al.*, *NAR*, 25:2745 (1997)). VDA analysis identified 85% of variants found by direct
 10 sequencing, while DHPLC identified 87% of the variants found by direct sequencing. In regions screened by both VDAs and DHPLC, the combination of the two methods identified 100% of the polymorphisms found by direct sequencing.

Overall, about one-third of individuals were screened with both methods, and one-third were screened with each of the two methods alone. (For some genes, the
 15 non-coding regions were screened only by DHPLC.) It is estimated that the false negative rate over the entire study to be about 15% for regions screened by one method, and negligible for sequences screened by both methods. The total number of true polymorphisms not identified is estimated to be less than 10%.

A SNP survey can be characterized in terms of either K , the observed
 20 number of variant sites, or p , the observed heterozygosity per bp. Because K increases with the number of chromosomes (n) studied and the total sequence length L , it is preferable to use the normalized number of variant sites

$$\hat{\theta} = K / \left(\sum_{i=1}^{n-1} i^{-1} \right) L \text{ which corrects for sample size. Under the neutral}$$

theory of molecular evolution and infinite sites model, θ and π are both estimators
 25 of the population genetic parameter $\theta = 4N\mu$ (Li, *Molecular Evolution*, Sinauer Associates (1997), Canada).

SNPs were found at a similar overall frequency in coding and non-coding regions. SNPs in coding region occurred at a frequency of 1 per 344 bp, corresponding to $\hat{\theta} = 5.47 \times 10^{-4}$ and $\pi = 5.07 \times 10^{-4}$. Interestingly, SNPs were
 30 observed in non-coding DNA at a similar frequency of 1 per 397 bp. The

normalized number of variant sites was $\theta = 4.93 \times 10^{-4}$, and the mean heterozygosity (π) = 5.05×10^{-4} (Figure 4). Calculations of π involve allele frequencies. Polymorphisms identified by DHPLC alone were excluded because we did not sequence all of the samples showing a variant DHPLC pattern and thus could not be certain of allele frequency. The estimates of π were thus based on 411 of 545 polymorphisms. Although the VDAs were designed for polymorphism discovery rather than genotyping, the estimated allele frequencies proved to be quite accurate. Specifically, genotyping assays (employing single-base extension assays) for 25 SNPs yielded allele frequencies that differed by an average of only 2% from those estimated on the basis of genotypes inferred from the VDA. For both classes, the similar values for θ and π is consistent with a population evolving according to neutral expectations.

The 395 cSNPs were roughly equally divided between synonymous (203 cSNPs) and non-synonymous (192 cSNPs) changes. Since approximately two-thirds of random mutations would alter an amino acid, the fact that non-synonymous cSNPs comprise slightly less than half of the cSNPs implies strong selection against amino-acid altering changes. To address this issue more directly, the nucleotide diversity was examined at four-fold degenerate sites, two-fold degenerate sites, and non-degenerate sites. Changes at four-fold degenerate sites produce only synonymous changes, while those at non-degenerate sites are always non-synonymous. Nucleotide diversity (θ) was 9.64×10^{-4} at four-fold degenerate sites, 6.85×10^{-4} at two-fold degenerate sites, and 3.70×10^{-4} at non-degenerate sites. Assuming that mutations occur at an equal rate at both classes of sites, non-synonymous variants survive to be detected in such a survey at only 38% of the rate of synonymous changes.

The force of selection is also evident in comparing non-synonymous cSNPs causing a non-conservative amino acid alteration with those causing a conservative amino-acid change. Conservative and non-conservative amino acid substitutions were defined for this analysis according to the BLOSUM62 matrix, used in sequence comparison (S. Henikoff and J. G. Henikoff, *PNAS*, 89:10915 (1992)). Conservative changes were those having a positive or neutral sign in the matrix, while non-conservative changes were those having a negative value. Non-conservative

cSNPs represent only 36% of the non-synonymous cSNPs, whereas randomly distributed mutations would be expected to produce a higher proportion (52%) of non-conservative changes. The proportion of non-synonymous SNPs expected to cause a non-conservative amino acid substitution was determined based on the actual codon usage in the 106 genes studied, the known frequencies of transitions and transversions, and the definition of non-conservative changes employed in the BLOSUM62 matrix. This implies that non-conservative cSNPs survive to be detected in such a survey at only about half of the rate of conservative, non-synonymous cSNPs.

The various types of SNPs differ not only in the rate of their occurrence, but also in the frequency of their minor alleles. This can be seen in several ways. When SNPs are classified according to whether the frequency of the minor allele was high ($\geq 15\%$), intermediate (5-15%) or low ($\leq 5\%$), it is clear that the non-synonymous cSNPs were enriched in low frequency alleles compared to the rest of the collection (Figure 1). The distribution of non-synonymous allele frequencies was significantly different than that of synonymous changes ($p=0.02$, Kolmogorov-Smirnov test). Indeed, more than half (58%) of non-synonymous cSNPs were found at a frequency below 5%, with this effect evident for both conservative and non-conservative substitutions.

The effect of selection can also be inferred by considering the average frequency of the minor allele: it is 8% for non-conservative cSNPs, 11% for conservative but non-synonymous cSNPs, and 14% for both synonymous cSNPs and non-coding SNPs. In addition, the lower allele frequency of non-synonymous cSNPs is reflected in the fact that the heterozygosity π is lower than the normalized rate of variant sites $\hat{\theta}$ for this class of SNPs (Figure 4). This divergence is in the direction predicted by the action of purifying selection, although it falls short of statistical significance. Tajima's D was non-significant. (F. Tajima, *Genetics*, 123:545 (1989).

The distribution of SNPs among the 106 genes was explored, with an eye toward detecting differential effects of selection among genes. The number of cSNPs per gene ranged from 37 for Factor V to 0 for thirteen of the genes, and the normalized rate, $\hat{\theta}$, similarly showed considerable variation (Figure 2). The

observed variation in nucleotide diversity is similar in magnitude to that observed for *Drosophila* (E. N. Moriyama and J. R. Powell., *Mol. Biol. Evol.*, 13:261 (1996)). Variation among genes could be due to many factors (D. J. Begun and C. F. Aquadro, *Nature*, 356:519 (1993); Nachman *et. al.*, *Genetics*, 150:1133 (1998)).

- 5 The fact that non-synonymous cSNPs show a somewhat wider variation than synonymous cSNPs (the coefficient of variation is 20% larger for the former class) is consistent with differences in selective constraints among loci, but the difference falls well below statistical significance. A variety of population genetic tests are available for testing selection at individual loci (M. L. Wayne and K. L. Simonson, 10 *Trends and Ecology and Evolution*, 13:236 (1998)).

The age of a SNP allele has important implications for its use in human genetic studies. Recently-occurring SNP alleles are more likely to show extensive linkage disequilibrium (retention of the ancestral haplotype on which they arose) as compared to older SNPs. Such linkage disequilibrium can provide a powerful tool 15 in identifying disease genes (E. S. Lander, N.J. Schork, *Science*, 265:2037 (1994)). Although the precise age of the SNPs could not be assessed from these studies, characterization of which allele preceded human speciation and which arose thereafter was sought. To determine the ancestral human allele, each corresponding gene was sequenced from the common chimpanzee (*P. troglodytes*). Each assay 20 used in the human survey was amplified from a single chimpanzee (DNA gift of Kristin Ardlie) and subjected to dye-primer sequencing on both strands. A single chimpanzee sample will accurately reveal the ancestral allele except in cases where the site has mutated and fixed during the chimpanzee evolution or is polymorphic in the chimpanzee population and happened to be homozygous for the non-ancestral 25 allele. These two cases are quite rare (probably less than 2%) and thus have been neglected for the purpose of estimating overall rates. A human allele was considered to be ancestral if it was present in the homozygous state in the chimpanzee sample. A total of 136 kb of chimpanzee sequence was obtained, revealing an inter-species divergence of 0.6% in the regions studied.

- 30 An elegant result in theoretical population genetics predicts that the probability that a neutral allele represents the ancestral state should be equal to its frequency in the population (G. A. Watterson and H. A. Guess, *Theoretical*

Population Biology, 11:141 (1977)). The minor allele should thus represent the ancestral state in a predictable proportion of cases. The ancestral allele and minor allele frequency was determined for 267 of the reported SNPs. For 3 of the 267 SNPs, the chimpanzee was homozygous for a third allele differing from both of the
5 current human alleles. This is consistent with the overall 0.6% nucleotide sequence divergences seen between human and chimpanzee. Among polymorphisms with a minor allele frequency below 10%, the average allele frequency was 3% and the proportion that was ancestral was 7% (11/158) of cases. Among polymorphisms with minor alleles exceeding 10%, the mean frequency was 28% and the proportion
10 that were ancestral was 32% (35/109). These results thus agree remarkably well with the theoretical prediction, providing the first reported test of this prediction in humans. It therefore follows that the minor SNP allele need not be the younger allele; this has implications for linkage disequilibrium mapping.

The distribution of SNPs among Caucasian, African-American, African and
15 Asian samples was also examined. Although the vast majority of SNPs were seen in multiple groups, there was a statistically significant excess of SNPs that were seen in only one of the sub-groups. The probability that a SNP occurring $k > 1$ times in an overall sample of n individuals would be found entirely within a given subset of m individuals is $B(n,k)/B(m,k)$, where $B(x,y)$ is the binomial coefficient $x!/(x-y)!y!$. In
20 this fashion, the probability that each individual SNP would be confined to a particular ethnic subgroup within the sample was calculated and these probabilities were summed to obtain the number of SNPs expected to be confined to the group within the sample. The fact that a SNP is found only within one group in the sample does not necessarily imply that it is private to that group within the general
25 population, owing to the small sample size, but it can be used as an indication of substructure. The number of SNPs with $k > 1$ confined to the, African-Americans, African Pygmies, Caucasians, and Asians was 17, 17, 12, and 9, as compared to expectations of 3.02, 1.34, 8.62, and 1.81. Not surprisingly, the greatest excess was seen for SNPs found in the African-American and African samples. The presence of
30 population substructure implies that construction of a comprehensive SNP database should employ a diverse set of DNA samples.

The results of this survey provide a fundamental description of sequence variation in the coding regions of human genes. These data indicate that two copies of a gene chosen from the human population will differ by roughly one base in 2 kb, corresponding to somewhat less than one heterozygous base within the coding region of a typical gene. In general, there are only a handful of such cSNPs per gene that exhibit allele frequencies of at least a few percent. Accounting for both the different rate and frequency of non-synonymous SNPs, only about 40% of these observed changes will alter the encoded amino acid. The action of purifying selection during human evolution is evident from the comparatively lower rate of non-synonymous cSNPs, and especially of those that create a non-conservative change. It is clear that non-synonymous cSNPs not only occur less often, but also have lower minor allele frequencies: 60% of non-synonymous cSNPs, the class likely to have the most dramatic effects on proteins, display a minor allele frequency below 5%.

The relative rarity of cSNPs has important implications for efforts to produce large catalogues of human variants. It has been proposed that most human SNPs could be found by performing shotgun sequencing on a handful of individuals (J. L. Weber and E. W. Myers, *Genome Research*, 7:401 (1997); J. C. Venter *et. al.*, *Science*, 280:1540 (1998)). Although such a project will surely identify many SNPs, results described herein suggest that the small sample size will likely fail to identify the vast majority of cSNPs likely to have the most important biological consequences, owing to their lower average allele frequencies. A comprehensive collection of the common, non-conservative cSNPs may require surveying 50-100 chromosomes. Because coding sequence represents only about 3% of the genome, it may prove inefficient to obtain such deep coverage of cSNPs by shotgun sequencing of genomic DNA. Instead, it may be more efficient to perform shotgun sequencing on cDNA libraries from multiple individuals or to amplify genes from multiple individuals, as done here.

Interestingly, a similar rate of polymorphism in coding and non-coding DNA was found. Furthermore, the observed rate of nucleotide diversity at four-fold degenerate sites was nearly twice that in adjacent non-coding regions, and over twice that at non-degenerate sites (Figure 4). Similar results have been reported for

Drosophila (E. N. Moriyama and J. R. Powell., *Mol. Biol. Evol.*, 13:261 (1996)) and for a smaller human data set by Li and Sadler (R. M. Harding *et. al.*, *Am. J. Hum. Genet.*, 60:772 (1997); D. A. Nickerson *et. al.*, *Nature Genetics*, 19:233 (1998); W. H. Li and L.A. Sadler, *Genetics* 129:513 (1991)), who observed over three times
5 the nucleotide diversity at four-fold degenerate sites ($\hat{\theta} = 11 \times 10^{-4}$), as compared to that in both untranslated regions and non-degenerate sites ($\hat{\theta} = 3 \times 10^{-4}$). These observations suggest that non-coding DNA adjacent to coding regions may be functionally constrained to a surprising degree.

SNPs can be used to search for genes underlying complex traits in two
10 distinct ways: linkage disequilibrium (LD) studies and association studies (E. S. Lander, N.J. Schork, *Science*, 265:2037 (1994)). Genome-wide LD studies involve using a dense collection of SNPs as markers to search for an ancestral haplotype carrying a disease-susceptibility allele. Such studies cannot be undertaken without the availability of an extremely dense SNP map and their potential for success
15 depends sensitively on many population genetic assumptions. Association studies are more straightforward because they directly test the hypothesis that a specific SNP increases disease risk. They make few assumptions, and require only the availability of a suitable database of appropriate SNPs. In the near term, focusing on cSNPs is likely to be most productive inasmuch as the class is easily recognized (in
20 contrast to regulatory polymorphisms) and is likely to contain a significant proportion of the disease-susceptibility alleles.

The present invention relates to a gene which comprises a single nucleotide polymorphism (SNP) at a specific location. The gene which includes the SNP has at least two alleles, referred to herein as the reference allele and the variant allele. The
25 reference allele (prototypical or wild type allele) has been designated arbitrarily and typically corresponds to the nucleotide sequence of the gene which has been deposited with GenBank or TIGR under a given Accession number. The variant allele differs from the reference allele by one at least one nucleotide at the site(s) identified in Figures 5A-5Q. The present invention also relates to variant
30 alleles of the described genes and to complements of the variant alleles. The invention further relates to portions of the variant alleles and portions of complements of the variant alleles which comprise (encompass) the site of the SNP

and are at least 5 nucleotides in length. Portions can be, for example, 5-10, 5-15, 10-20, 5-25, 10-30, 10-50 or 10-100 bases long. For example, a portion of a variant allele which is 5 nucleotides in length includes the single nucleotide polymorphism (the nucleotide which differs from the reference allele at that site) and four

5 additional nucleotides which flank the site in the variant allele. These nucleotides can be on one or both sides of the polymorphism. Polymorphisms which are the subject of this invention are defined in Figures 5A-5QQQQQQQ with respect to the reference sequence deposited in GenBank under the Accession number indicated. For example, the invention relates to a portion of a gene (e.g., AADC) having a
10 partial nucleotide sequence as shown in Figures 5A-5QQQQQQQ comprising a single nucleotide polymorphism at a specific position. The reference nucleotide for AADC is shown in column 3 and the variant nucleotide is shown in column 4 of Figures 5A-5QQQQQQQ. The nucleotide sequences of the invention can be double- or single-stranded.

15 The invention further provides allele-specific oligonucleotides that hybridize to a gene comprising a single nucleotide polymorphism or to the complement of the gene. These oligonucleotides can be probes or primers.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the
20 polymorphic sites shown in Figures 5A-5QQQQQQQ. Optionally, a set of bases occupying a set of the polymorphic sites shown in Figures 5A-5QQQQQQQ is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the
25 polymorphic site or sites in the individuals tested.

An oligonucleotide of this invention can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the
30 polymorphic sites shown in Figures 5A-5QQQQQQQ. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any

position of the segment. The segments can be from any of the allelic forms of DNA shown in Figures 5A-5Q.

As used herein, the terms "nucleotide" and "nucleic acid" are intended to be equivalent. The terms "nucleotide sequence", "nucleic acid sequence", "nucleic acid molecule" and "segment" are intended to be equivalent.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen *et al.*, *Science* 254, 1497-1500 (1991). Probes can be any length suitable for specific hybridization to the target nucleic acid sequence. The most appropriate length of the probe may vary depending upon the hybridization method in which it is being used; for example, particular lengths may be more appropriate for use in microfabricated arrays, while other lengths may be more suitable for use in classical hybridization methods. Suitable probes and primers can range from about 5 nucleotides to about 30 nucleotides in length. For example, probes and primers can be 5, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 25, 26, 28 or 30 nucleotides in length. The probe or primer preferably contains at least one polymorphic site occupied by any of the possible variant nucleotides. The nucleotide sequence can correspond to the coding sequence of the allele or to the complement of the coding sequence of the allele.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (*e.g.*, in the presence of four different nucleoside triphosphates and an agent for polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template. The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5'

end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same
5 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred
10 markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide
15 repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous
20 for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

By altering amino acid sequence, SNPs may alter the function of the encoded proteins. The discovery of the SNP facilitates biochemical analysis of the variants and the development of assays to characterize the variants and to screen for
25 pharmaceutical that would interact directly with on or another form of the protein. SNPs (including silent SNPs) may also alter the regulation of the gene at the transcriptional or post-transcriptional level. SNPs (including silent SNPs) also enable the development of specific DNA, RNA, or protein-based diagnostics that detect the presence or absence of the polymorphism in particular conditions.

30 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site

is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than
5 pure red blood cells) is suitable. For example, convenient tissue samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

10 Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. *See generally PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucleic Acids Res.* 19, 4967 (1991); Eckert *et al.*, *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren *et al.*, *Science* 241, 1077
20 (1988), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and
25 double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis, sometimes referred to as de novo
30 characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target

sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki *et al.*, *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)).

5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita *et al.*, *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

II. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard *et al.*, National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

Homozygote: $p(\text{AA}) = x^2$

Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$

Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$

Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

- The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + y^4 + z^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

- The cumulative probability of identity ($cum\ p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

$$cum\ p(ID) = p(ID1)p(ID2)p(ID3)... p(IDn)$$

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$cum\ p(nonID) = 1 - cum\ p(ID).$$

- If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

B. Paternity Testing

- The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots p(\text{non-exc}n)$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending

on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of diseases which can be treated or diagnosed as described herein include, but are not limited to, bradyarrhythmias, tachyarrhythmias, heart failure, such as congestive heart failure, congenital heart disease, rheumatic fever, valvular heart disease, cardiomyopathies, myocarditides, pericardial diseases, cardiac tumors, cardiac manifestations of systemic diseases, and traumatic cardiac injury. Other disorders include atherosclerosis, acute myocardial infarction, ischemic heart disease, hypertensive vascular disease, disorders of the aorta, vascular diseases of the extremities, vessel wall disorders, such as various forms of thrombocytopenia, von Willebrand's disease and drug-induced platelet dysfunction, and homeostatic disorders relating to vessel disease and associated bleeding. Also suitable are thrombotic thrombocytopenic purpura, hemolytic-uremic syndrome, Henoch-Schönlein purpura, capillary fragility, vascular purpura, metabolic and inflammatory disorders, such as those induced by rickettsiae and certain drugs, such as sulfonamides, aortic aneurysm, aortic dissection, aortic occlusion, aortitis, atherosclerosis, coronary artery disease, angina, myocardial infarction, thrombosis, hemostatic and coagulation disorders, hypertension and hypotension. Other disorders include transplant accelerated vascular restenosis following balloon angioplasty, Raynaud's disease and acrocyanosis.

Additional disorders include, but are not limited to, disorders of neurodegeneration characterized by astrocyte hypertrophy including gliosis, Pick's disease, aceroplasminemia, portal-systemic encephalopathy, frontal lobe dementia and inherited and acquired ataxias, neurodegenerative diseases of other etiology including progressive supranuclear palsy, primary progressive aphasia, cortical basal degeneration, Alzheimer's disease, Huntington's disease, and Parkinson's disease, retinitis pigmentosa and amyotrophic lateral sclerosis. Other disorders include epilepsy, stroke, defects of neural migration and differentiation, including Miller-Dieker lissencephaly syndrome, and cancer of the brain including astrocytomas and gliomas, as well as psychological disorders such as schizophrenia.

Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

The correlation of one or more polymorphisms with phenotypic traits can be facilitated by knowledge of the gene product of the wild type (reference) gene. The genes in which cSNPs of the present invention have been identified are genes which have been previously sequenced and characterized in one of their allelic forms.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods such as a χ^2 -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz *et al.*, US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is

composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used
5 as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus
10 associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning
15 gene(s) responsible for the trait. See Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller *et al.*, *Cell* 51, 319-337 (1987); Lander *et al.*, *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

20 Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem *et al.*, *Science* 245, 1073-1080
25 (1989); Monaco *et al.*, *Nature* 316, 842 (1985); Yamoka *et al.*, *Neurology* 40, 222-226 (1990); Rossiter *et al.*, *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus
30 the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company,

Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci
5 unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer
10 programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith *et al.*, *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150
15 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of
20 +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the
25 remaining non-excluded chromosomal locations.

III. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in Figures 5A-5Q, column 11, in which the polymorphic position is
30 occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the

prototypical amino acid sequences encoded by nucleic acid sequences shown in Figures 5A-5QQQQQQQ, column 11, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in Figures 5A-

- 5 5QQQQQQQ. That position is occupied by the amino acid coded by the corresponding codon in any of the alternative forms shown in Figures 5A-5QQQQQQQ.

- Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a
- 10 eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors
- 15 can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

- The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means
- 20 include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, *e.g.*, mouse, CHO, human and monkey cell lines and
- 25 derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

- The protein may be isolated by conventional means of protein biochemistry
- 30 and purification to obtain a substantially pure product, *i.e.*, 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles*

and Practice, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

- 5 The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan *et al.*,
10 "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous
15 recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

- In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate the
20 interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

- 25 Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*,
30 Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and

lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

IV. Kits

5 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific
10 oligonucleotide probes for detecting at least 10, 100 or all of the polymorphisms shown in Figures 5A-5Q. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and
15 the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the diagnosis or
20 monitoring of diseases, such as coronary artery disease, diabetes, coagulation disorders, lipid metabolism disorders, energy metabolism disorders, diseases of the blood, blood vessels and cardiovascular system, and infection by microorganisms, as well as psychological disorders (e.g., bipolar disorder, psychiophrenia). The invention further provides for the use of any of the nucleic acid segments in the
25 manufacture of a medicament for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled
30 in the art that various changes in form and details may be made therein without

departing from the spirit and scope of the invention as defined by the appended claims.

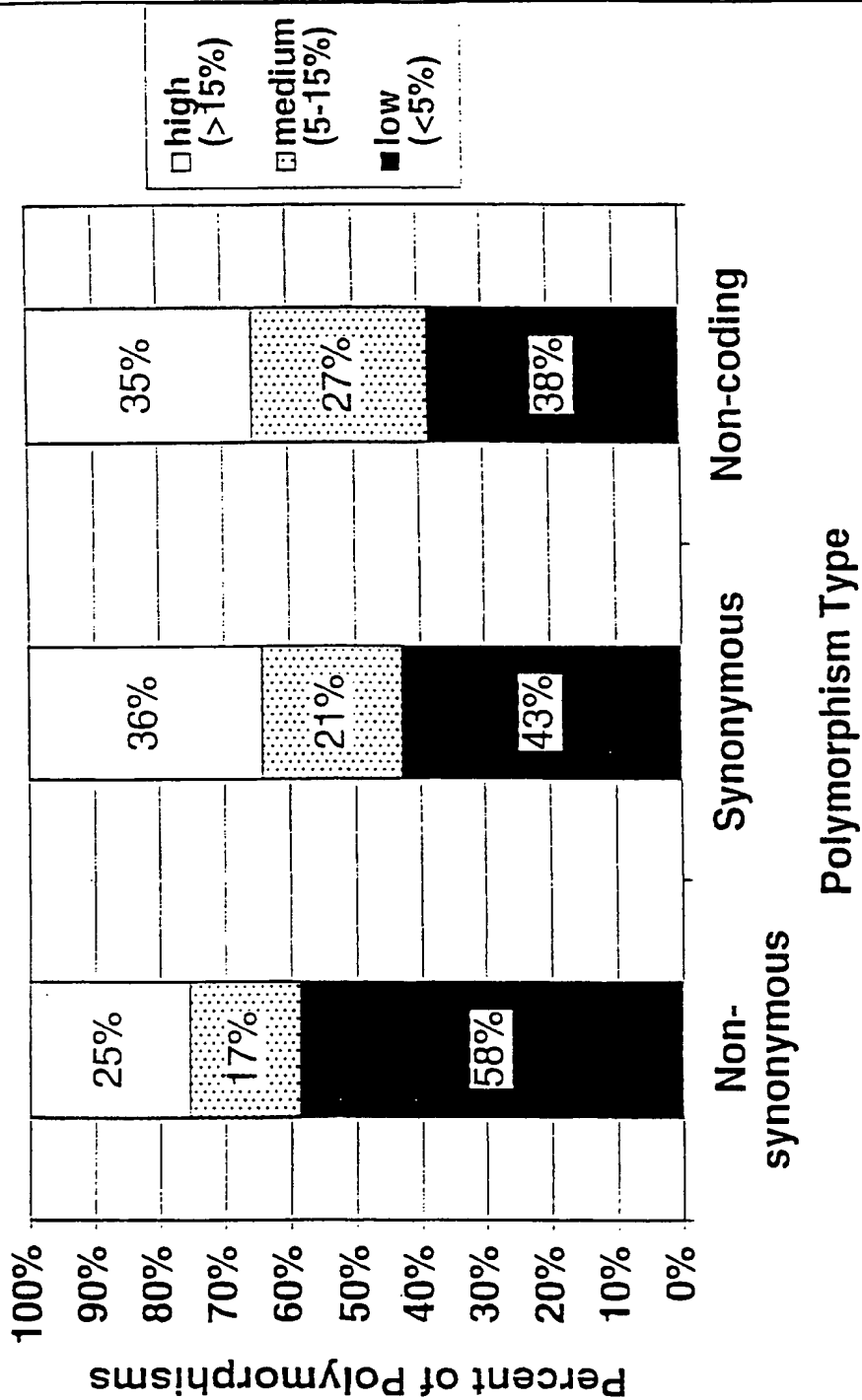
CLAIMS

What is claimed is:

1. A nucleic acid molecule selected from the group consisting of the genes listed in Figures 5A-5Q, wherein said nucleic acid molecule is at least 5 nucleotides in length and comprises a polymorphic site identified in Figures 5A-5Q, wherein a nucleotide at the polymorphic site is different from a nucleotide at the polymorphic site in a corresponding reference allele.
2. A nucleic acid molecule according to Claim 1, wherein said nucleic acid molecule is at least 10 nucleotides in length.
3. A nucleic acid molecule according to Claim 1, wherein said nucleic acid molecule is at least 20 nucleotides in length.
4. A nucleic acid molecule according to Claim 1, wherein the nucleotide at the polymorphic site is the variant nucleotide for the gene listed in Figures 5A-5Q.
5. An allele-specific oligonucleotide that hybridizes to a portion of a gene selected from the group consisting of the genes listed in Figures 5A-5Q, wherein said portion is at least 5 nucleotides in length and comprises a polymorphic site identified in Figures 5A-5Q, wherein a nucleotide at the polymorphic site is different from a nucleotide at the polymorphic site in a corresponding reference allele.
6. An allele-specific oligonucleotide according to Claim 5 that is a probe.
7. An allele-specific oligonucleotide according to Claim 5, wherein a central position of the probe aligns with the polymorphic site of the portion.

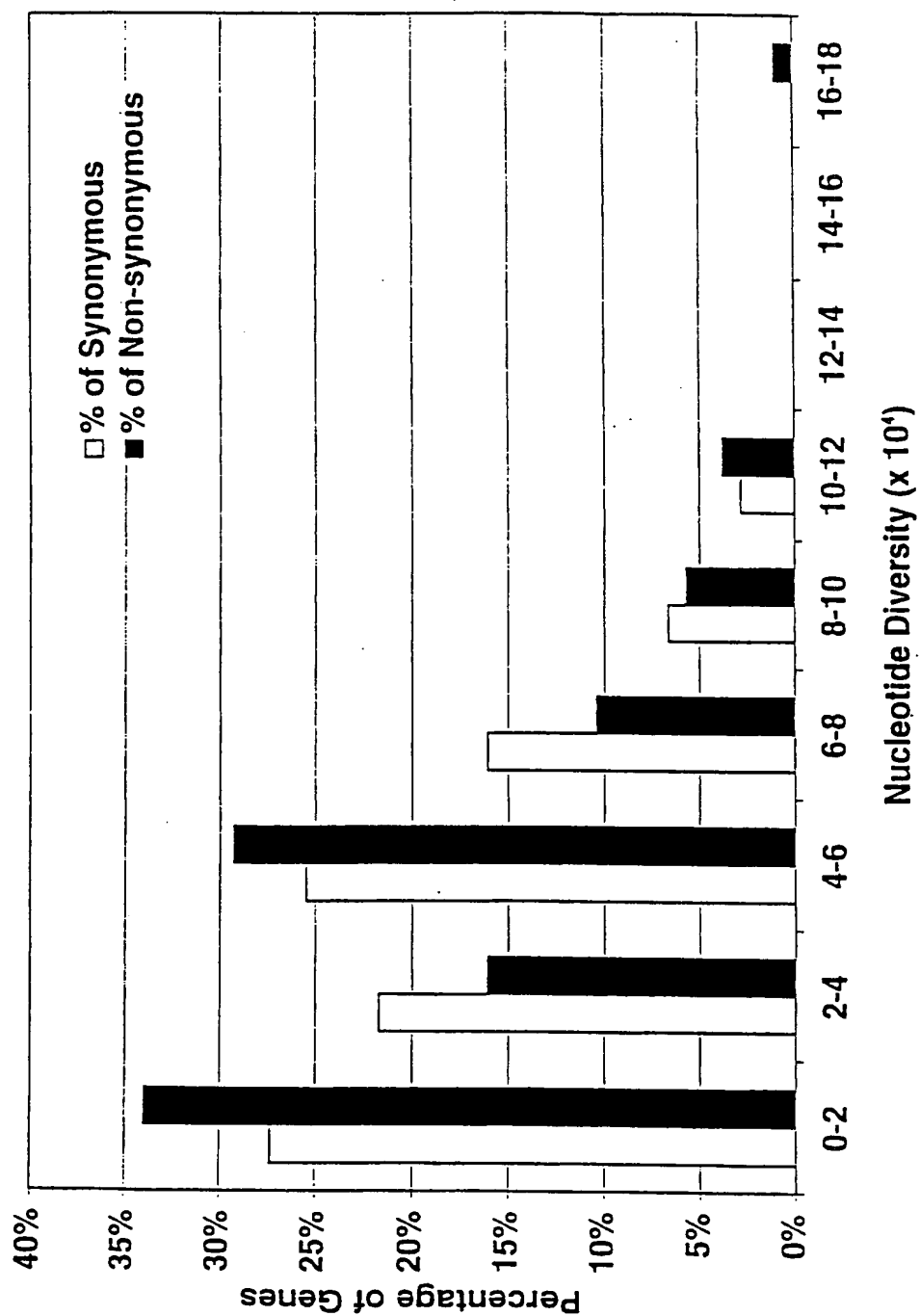
8. An allele-specific oligonucleotide according to Claim 5 that is a primer.
9. An allele-specific oligonucleotide according to Claim 8, wherein the 3' end of the primer aligns with the polymorphic site of the portion.
10. An isolated gene product encoded by a nucleic acid molecule according to Claim 1.
11. A method of analyzing a nucleic acid sample, comprising obtaining the nucleic acid from an individual sample; and determining a base occupying any one of the polymorphic sites shown in Figures 5A-5Q. Q. Q. Q. Q. Q. Q. Q. Q.
12. A method according to Claim 11, wherein the nucleic acid sample is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

FIG. 1



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FIG. 2



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Gene	coding bp screened	No. Synonymous polymorphisms	No. Non- synonymous polymorphisms	Non-coding bp screened	No. Non-coding polymorphisms
AADC	1229	0	2	311	0
ADORA2	332	0	1	75	0
AHC	1413	0	0	63	1
ANX3	929	2	4	725	6
APOD	570	1	3	383	1
AR	2759	3	1	300	0
AT3	1357	3	0	121	0
BDNF	744	0	1	212	0
CD36	1209	1	1	252	0
CETP	1397	4	4	299	0
CGA	349	1	0	235	0
CLanalog	1461	3	2	12	0
CNTF	603	0	1	154	0
COMT	783	2	1	241	1
CRH	51	0	0	745	3
CYP11A	1556	1	1	547	0
CYP11B1	1410	7	7	496	9
CYP11B2	1512	7	8	906	4
CYP17	1395	3	0	36	0
CYP21	1488	5	11	542	7
DBH	1266	0	2	49	0
DRD1	1341	1	0	81	0
DRD2	1032	2	0	1379	3
DRD3	719	0	1	145	0
DRD5	1408	2	1	34	0
F10	1369	3	2	416	1
F11	1878	7	4	1312	2
F13A1	2199	3	6	948	4
F13B	1952	4	6	2339	4
F2	1740	3	2	292	0
F2R	1202	2	1	13	0
F3	875	0	1	92	0
F5	6564	13	16	1542	8
F7	1262	4	2	1209	2
F9	1364	0	1	1062	2
FGA	1935	2	2	490	0
FGB	1476	7	3	1057	0
FGG	1252	0	2	1392	2
FSH	355	1	1	44	0
FSHR	1683	1	3	0	0
GABRB1	1425	5	0	804	2
GAP43	675	1	1	79	0
GH1	644	0	1	426	5
GHR	1765	1	6	391	1
GNRHR	237	0	1	513	0
GP1BA	1881	2	2	48	0
GP1BB	1238	0	0	73	0
GP5	1683	0	0	52	0
GP9	534	1	0	143	0
GRF	224	0	0	239	0
GRIN1	1681	1	0	553	0
GRL	2334	4	3	4028	5
HCF2	1500	3	3	64	1

FIG. 3A

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Gene	coding bp screened	No. Synonymous polymorphisms	No. Non- synonymous polymorphisms	Non-coding bp screened	No. Non-coding polymorphisms
HMGCR	1724	0	1	12	1
HSD3B1	1122	3	2	653	1
HSD3B2	1122	1	1	723	2
HTR1A	1272	1	0	1189	1
HTR1D	1134	1	1	46	0
HTR1DB	1173	2	0	85	1
HTR1E	1098	1	1	70	0
HTR1EL	1101	1	0	46	0
HTR2A	1398	2	3	1709	9
HTR2C	1245	0	1	138	0
HTR5A	1062	2	0	34	0
HTR6	437	1	0	34	0
HTR7	1279	0	0	138	0
IGF1	630	0	0	7250	8
IGF2	546	0	0	610	1
ITGA2B	2833	4	3	707	0
ITGB3	2131	4	3	163	0
KLK2	297	0	1	279	2
LCAT	1289	1	2	90	0
LDLR	2101	7	3	38	0
LIPC	1471	4	3	754	4
LPL	409	1	1	48	0
MAOA	1032	1	0	69	0
MAOB	980	1	0	135	0
MPL	1748	1	2	903	1
NGFB	726	1	1	1186	5
NOS1	127	0	0	56	0
NT3	774	1	0	150	0
NTRK1	1961	5	2	1106	0
PACE	1500	2	0	1095	4
PAI1	1171	1	2	911	1
PAI2	1248	5	4	915	5
PC1	1881	1	3	456	1
PCI	1221	5	5	576	4
POMC	132	0	0	520	0
PRL	633	1	1	180	1
PROC	1334	3	0	114	0
PROS1	1868	1	0	557	0
PTAFR	1029	0	2	13	0
PTH	348	1	0	230	2
PTHLH	634	0	0	2342	13
SELP	2096	5	8	14	0
SHBG	1209	1	3	494	1
SLC6A1	1388	2	0	547	2
SLC6A3	1496	6	1	205	0
SLC6A4	1623	1	2	824	1
TBXA2R	1006	1	0	12	0
TBXAS1	1605	1	6	1411	1
TFPI	806	0	1	139	0
TH	965	1	1	104	0
THBD	1728	0	0	26	0
THPO	1049	0	0	632	2
VLDLR	2391	3	1	850	2
ALL GENES	135823	203	192	59552	150

FIG. 3B

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Polymorphism rates for different classes of sites. Nucleotide diversity ($\hat{\theta}$) and heterozygosity (π) are expressed $\times 10^4$.

Polymorphism Type	bp screened	No. polys	Adjusted for frequency of sites*			
			Frequency (SNP/bp)	$\hat{\theta}$	π	π
Non-coding	59,552	150	1/397	4.93 \pm 1.24	5.05 \pm 2.40	
Coding	135,823	395	1/344	5.47 \pm 1.32	5.07 \pm 2.40	
synonymous		203	1/669	2.81 \pm 0.68	2.98 \pm 1.42	9.84 \pm 2.38
non-synonymous		192	1/707	2.66 \pm 0.64	2.06 \pm 0.98	3.73 \pm 0.90
conservative		122	1/1113	1.69 \pm 0.41	1.44 \pm 0.68	4.94 \pm 1.19
non-conservative		70	1/1940	0.97 \pm 0.23	0.63 \pm 0.30	2.61 \pm 0.63
four-fold degenerate sites	21,645	111	1/195	9.64 \pm 2.32	9.26 \pm 4.40	
two-fold degenerate sites	34,294	125	1/274	6.85 \pm 1.65	5.33 \pm 2.53	
non-degenerate sites	79,659	157	1/507	3.70 \pm 0.89	2.52 \pm 1.19	
Total	195,375	545	1/357	5.31 \pm 1.28	5.01 \pm 2.38	

* The number of synonymous sites was calculated as the sum of four-fold degenerate sites and half the number of two-fold degenerate sites; the number of non-synonymous sites is the sum of the non-degenerate sites and half the two-fold degenerate sites. The number of conservative and non-conservative sites is estimated as the proportion of non-synonymous sites at which a nucleotide substitution would create a conservative or non-conservative substitution, calculated as in footnote 21.

FIG. 4

[illegible]

FIG. 5B

[illegible]

FIG. 5C

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
ANX3u9	ANX3	G	A	S	N	cds	GE443	GATGTCATTTT GAACCAATG	TGTAACTGGC TCATTTGCTTC	CATGTCATTTTGAACCAATGgactttccagtaattctcttaggttggacacccgaggacagtaaa gagattatccagacttta(g/a)cccatcagtgagatctgaagactatcgaagaacatcagagag aatTggTgagTgattttatcaattctcttttaattgttGAAGCAATACAGCAAGTTTACA
AP0D7	AP0D	T	C	F	S	cds	GE320	AGAAGGCTCAG AATGACAAC	CAGCATAAATTA CATTCGAACCTT GTAG	AGAAGGCTCAGATGACACACCCagctgctttggcttcccgagctccaggttcccttccagcc accagccccagaatggtgatcgtcgtctgctttccagacttccagactgctggtcctt(c/c)cggt gcgcagaggagacaagattctcatctgggaagtgcctcaatccctcggtgcaggaagaatttga cgtgaataggttaaaggcgaacctcccgcttgggttctgctccctcgctgtaataagcgcttCTA CAGGTTCAATGTAATATGCTG
AP0D8	AP0D	C	G	-	-	noncoding	GE371	CAGCCTTCTTG TGTTGTCTG	TGCTGGTGTAT TGCTTTGTCT	CAGCCTTCTTGTTGCTGCTGagattttcttgcctctctctccatcaatgctgctctctctc gtctcagttatgcatcagcacctgactggacttggccagcagactatgagaactatgctctc tgattctctgacctcgaatcatcacaacttttccagtgattttcttggtatttggcaagaac cctaatctctccagaacagtgagacttcaaaaaatactcagacttcaataacactgattg caagaaatgacggtcacagacaggtgaactgccccagctctcgttaaccaggttctacagga ggctgacccactccatgttaacttctgcttcttccctaccaccccc(c/g)ccataaa GACAAACCAATCAACACGGA
AP0D9	AP0D	C	A	-	-	noncoding	GE371	CAGCCTTCTTG TGTTGTCTG	TGCTGGTGTAT TGCTTTGTCT	CAGCCTTCTTGTTGCTGCTGagattttcttgcctctctctccatcaatgctgctctctc gtctcagttatgcatcagcacctgactggacttggccagcagactatgagaactatgctctc tgattctctgacctcgaatcatcacaacttttccagtgattttcttggtatttggcaagaac cctaatctctccagaacagtgagacttcaaaaaatactcagacttcaataacactgattg caagaaatgacggtcacagacaggtgaactgccccagctctcgttaaccaggttctacagga ggctgacccactccatgttaacttctgcttcttccctaccaccccc(c/a)A GACAAACCAATCAACACGGA
AP0Du1	AP0D	A	T	E	V	cds	GE304	CTGCGTCTGCA CGACAATG	ACCAGTCACT CTCGCTCA	CTGCGTCTGACGACCAATGggagaagaattgacggttccccagagaacacaggggtttgtcTgc ttgtgtctctcagtaattctgggaagatggtacgaataatgagaagatccccacactttg(a/t) TgaatggacgctgcatccagggccactactcactaaTgggaacacaggaagatcaaatgttaaac caggagttgaggtgagtggtggtctgTgggctcgggccagggctgTggagTgcTACGACAGTGA CTGGGT
AP0Du2	AP0D	C	T	D	D	cds	GE320	AGAGGCTCAG AATGACAAC	CAGCATAAATTA CATTCGAACCTT GTAG	AGAGGCTCAGATGACACACCCagctgcttttggcttcccgagctccaggttcccttccagcc accagccccagaatggtgatcgtcgtctgctttccgactggctggcctctctggTggg cagagggacagcatctcatctgggaagtgcctcaactcccggtgcaggaagaatttga(c/t) TgtgaaTaaagTaaaggcgaacctcccgcttTgttttctgctcccgctgtaataagcgcttCTA CAAGTTCAATGTAATATGCTG
AP0Du3	AP0D	T	S	A	A	cds	GE286	GCTTATTTGGCT TTCAATGAGTT GT	TGCTCAGGAA TTCTCCAGC	GCTTATTTGGCTTTCAATGAGTTGTTTTtttttctctctctctctctctctctctctctctct aactcactgcagagctgaggaactgtgaaTcaaatcgaaggtggaagccccccaggttaactctca cagagctgcacagctggaagTtaagtttT(g)ccgtgtgtaagtatacctatctccagggg atctcagggacaggaataTgcaactggaagctagcgccccggCTTGGAGAAATTCCTGAGACA
AP0Du4	AP0D	C	T	S	L	cds	GE371	CAGCCTTCTTG TGTTGTCTG	TGCTGGTGTAT TGCTTTGTCT	CAGCCTTCTTGTTGCTGCTGagattttcttgcctctctctccatcaatgctgctctctc gtctcagttatgcatc(c/t)ggccagcgtactggatctccgctccagcagactatgagaactatgctc ctcgtgtattctcgtacctgcatcacaacttttccagTgggattttgcttggtactctggcaag aaacccctaactcctccagaacagtgagacttctcaaaaaatactcgtacttctaataacactg atgtcagaagaaatgacggttcacagacaggtgaactgccccagctctcgttaaccaggttctaca ggaggtgacccactccatgttaacttctgcttcttccctaccaccccccccccaaa GACAAACCAATCAACACGGA

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Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
ANX3u10	ANX3	T	G	L	R	cds	GE447	AAAGATATTT CAACATTTTTC C	TGATGACTTGG TCAAAACC	AAAGATATTTTCCCTTGGTCTTTTGGATTTAGGAGC(T/G)GAAAGATGACTTGA AGGATGATCTCTCTGGCCACTCTGAGCATCTCATGCTGGCTGAGCTCCAGCAGCTCTT GATGCAAGCAGCTCAAGAAATCCATGAAGGTATGAGCCCCCACAAGCCATTCTGCCAGGGT TTGACCAAGTCATCA	210
ANX3u11	ANX3	A	G	P	P	cds	GE447	AAAGATATTT CACATTTTTC C	TGATGACTTGG TCAAAACC	AAAGATATTTTCCCTTGGTCTTTTGGATTTAGGAGCTGAAAGTGAAGGG TGAATCTCTGGCCACTCTGAGCATCTCATGCTGGCTGAGCTCCAGCAGCTCTT GATGCAAGCAGCTCAAGAAATCCATGAAGGTATGAGCCCCCACAAGCCATTCTGCCAGGGT TTGACCAAGTCATCA	210
ANX3u12	ANX3	T	G	L	R	cds	GE441	AAAGAAATA ATTGTGTCTCT AATATC	TGTAATAACA CATACACACA AAGG	AAAGAAATAATTGTGCTCTTAATATCCTCTCTGTGAATAGATCTCTATAAAGCTGGTGA AACAGATGAGGGGACGAGATGAAGCAAAATCTCACTGAGATCC(T/G)GTGTTAAAGGAGCTTCTC AATTAACCACTAAGTACAGTACAACTCCATCAATCTTGTGTTGTTGTTTATCA	189
ANX3u13	ANX3	A	G	T	T	cds	GE460	ATTCAAAATGT CTCAACTGC	CTGAGTTAAAG CAAGTGCA	ATTCAAAATGTCTCAACTGCGTGTCTTAAATAATTTGTGGTCTCTTTTGAATTTGATGA ATACAGAAATA(T/A)CAGCCAAAGGACATTTGGACAGCATAAAGGGAGGAAATATCTGGGCAT TTTGAAGACTTACTGTGGCCAAATGAGTGAAGTCTGAGTGTGTAAGTAACTAAGTACTTTGCACT TGCTTTAACTCAG	208
ANX3u14	ANX3	T	A	I	N	cds	GE460	ATTCAAAATGT CTCAACTGC	CTGAGTTAAAG CAAGTGCA	ATTCAAAATGTCTCAACTGCGTGTCTTAAATAATTTGTGGTCTCTTTTGAATTTGATGA ATACAGAAATA(T/A)CAGCCAAAGGACATTTGGACAGCATAAAGGGAGGAAATATCTGGGCAT TTTGAAGACTTACTGTGGCCAAATGAGTGAAGTCTGAGTGTGTAAGTAACTAAGTACTTTGCACT TGCTTTAACTCAG	208
ANX3u2	ANX3	C	A	S	R	cds	GE425	CTTTTATAGGC GCGGA	AGCAACATTTG CTAAATATGTG	CTTTTATAGGCGGGAACAAAGAGTGCCTTGTATGAATCTTAACACCAGGAGAAAG(C/A) TAGGCAAAATGAAGGATATCTCTCAAGCTTATATACAGGTGCTTATTTCTGTCTTACCTCACC ACTGTCAACATATTTAGCCAAATGTGCT	160
ANX3u3	ANX3	C	T	P	L	cds	GE433	TTACTTTACTAT AGATTAACCCA ATTTC	TTTCCCAAGGG AATTAAGGG	TTACTTTACTATAGATTAACCAATTTCTATCTCCGTGAAGCTGAACATTTATTTGCTTTTGTACA GTAAATGTGTGAGGAACACG(C/T)GGCCCTTTTGAAGCAAGTGAATGAGCTTGAAGG TTGGTCTGGAAGTCTCATGTGCTTCTTGGCTTAAATTTCCCTTGGGAA	183
ANX3u4	ANX3	A	T	E	V	cds	GE444	TCTCTATGTTG CTTTGTGACCA AT	GACTTACTTTA ATTGCTGAATA TAGG	TCTCTATGTTGTTGTGACCAATGACATTTGTGTGTGAACACCTGCTCTTAAACAGGGTAT TGAAGTGTGATGATTTCTCTGAGCAAGTAAATGAGTGTGAGTCAAG(TA/T)AATGACCTTTG GACATCTGAACAGAGTCAAGAGCATTTGGCTATCTCTATTTCAAGCAATTAAGTATGTC	194
ANX3u5	ANX3	C	T	-	-	noncoding	GE439	TGATTCATTTA TGGTCTCCCAT T	GAAGTAAGGTG GAGCTGTTGG	TGATTCATTTATGTTGCTCCCATTTATTTATCTGATTTGTTTCTCATGATTTATTTCTTTT GCAAGAGATAATCTCTCAAGAGTCCAGATGGGCTTTTCCAAACAGCTCCACTTACTTC	189
ANX3u6	ANX3	G	T	-	-	noncoding	GE448	CTTTTGTTCAA GACAAATGTTG AC	TGATCTCTTAC TGCCTGTCA	CTTTTGTTCAGACAAATGTTGAGCAATAATTTGATGAATAAATCTTTG(T)TTCTCATTTAG GAACTGAGAGAAATGCTATCATGATCTGAGTGAAGGTCAAATGCAAGCGGAGCTGAT GTTAAGGAATATCAAGCAGCATATGGAAGGTGAAGTCAATCAATGACAGGAGTATGAGAT CA	197
ANX3u7	ANX3	A	T	E	D	cds	GE425	CTTTTATAGGC GCGGA	AGCAACATTTG CTAAATATGTG	CTTTTATAGGCGGGAACAAAGCAG(TA/T)GATGCTTGAATGAATCTTAACACCAGGAGAAAG CAGGCAAAATGAAGGATATCTCTCAAGCTTATATACAGGTGCTTATTTCTGTCTTACCTCACC ACTGTCAACATATTTAGCCAAATGTGCT	160
ANX3u8	ANX3	T	G	-	-	noncoding	GE443	GATGTCATTTT GAACCAATG	TGTAACTTGCC TCATTTGCTTC	GATGTCATTTTCAACCAATGAGCTTCAAGTATT(T/G)CTTCTAGGTGAGACCCAGGAGAA GTAAAGAGATATCCAGACTTAGCCCATGAGTGAAGCTATTCAGAAAGCAATCAGAGG AATTGGTGAATGATATTTCAATCTCTTCTTAAGTGAAGCAATCAAGCAATGAGTATCA	191

FIG. 5D

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[illegible]

FIG. 5H

[illegible]

FIG. 51.

[illegible]

FIG. 5K

[illegible]

FIG. 5L

[illegible]

FIG. 5M

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
CYP11B 1u15	CYP11B B1	G	A	R	H	cds	GE617	ATGGCACTCAG GGCATA	AGGGCTCTGGG TGTGTCC	ATGGCACTCAGGGCAAAAGGcagaggtgtgcatggcagtgccctggctgctccctgcaaggggcaca ggcactgggacacagagagccgggtgcccagcagtgctcccttgaagccatgccccagc lg/a ccaggcaacaggtggctgaggtgctgagatctggaggcagaggttatgaggaacct ggacctggaggtacacacagacctccaggaaactggggcccattttcagg aaagacctccctggc ccagctGGGAACACCCAGAGCCCT	285
CYP11B 1u16	CYP11B B1	C	T	D	D	cds	GE536	ATGGTCCCATTT CCAGCAC	AGCAAGAAC GCCACA	ATGGTCCCATTTCCAGCAAGGcctgctgtggccccccaggtacga c t tggggaggagcagg catgggtgtgtgtagctgcggaggagcgtgggaagctgcaacaggtggacagctgcatcccc acaggatgagcctggagccctgggtggctacagacacacatcgtgggcacaaaTGTGGCTGTTC TTGCT	200
CYP11B 1u17	CYP11B B1	G	A	L	L	cds	GE625	GGAGGAGGCA GGAGGC	GTGTCCCTTCC CCATAGCAC	GGAGGAGGCAAGGAGGcctgggtgtgctcagcagtgcatctcccccgaagcagcaac ttlg/a gctctttttggagagcgtgtggcctggttggccacagcccccaagttctggcagcttg aaatctccatgctcctggaggcagtggtcaatcccaatccagctcatgttcatgccccagag cctgtctcgtgacacagcccccaaggtgtggaagagcactttgagggcctgggaactgcatctcc agtaacgtgagggcaggggacccccggcagGTGCTATGGGAAGGAGAC	307
CYP11B 1u18	CYP11B B1	C	T	-	-	noncoding	GE570	TCCAGCACCA AAGCTGAG	GGCATCACCT CTCTGGGT	TCCAGCACCAAGGCTGTGAGggctgctccctc t gctccccgagtagggcacaactglatccag aaaatctacagaaactggcctcagccgcccctcaacagctacacagcagctgtggcggagctcct gttgaatgcggaaactgtgcceagatgccataaagccaaactctatgaaactcactgcaggagcg tggacacgggtcagggcggcgaacccagccccACCTAGAGAGGTATGCC	243
CYP11B 1u19	CYP11B B1	G	A	A	T	cds	GE582	CTCCTGTGCA GGTCTG	CTCCAGCAGG GGCCAG	CTCCTGTGCAAGGTCTGacctcagctgtgtctctcagcaggggtgttctcccttgcctgaac gctcttggagctggctcggaaaccccaagcctcagcagggccctggcagagagcctggcngcc g/a cagcagcatcagtgaaatccccaagaggaacacccagcagctncccttgcctgctggg ccctcaaggagaccttgcgggtgggtgctggctgagggcctccctgtggccCTGACCCCTGCTGGA G	261
CYP11B 1u2	CYP11B B1	A	G	E	E	cds	GE617	ATGGCACTCAG GGCATA	AGGGCTCTGGG TGTGTCC	ATGGCACTCAGGGCAAAAGGcagaggtgtgcatggcagtgccctggctgctccctgcaagggcaca ggcactgggacacagagagccgggttccccagagacagtgctgccccttgaagccatgccccagc gtccaggcaacaggtggctgaggtgctgcagatctggaggggaggggttatgaggacctgcac ctggaagtacacacagacctccaggga a g ctggggcccattttcagg aaagacctccctggc ccacgtGGGAACACCCAGAGCCCT	285
CYP11B 1u20	CYP11B B1	T	C	V	A	cds	GE531	ACAGGAAGCCC CATCCA	AGGTCTCTAGC TCGAGGGT	ACAGGAAGCCCATCCAGctgagggacctttctatgagtcccccccacctccaggtctctacctgt gggtctgttctggagcaggtgg c c gagctcagacttggcttcagaactaccacatccca gctgggg gagtgagcccaacACCTCTGAGCTGAGAACCT	171
CYP11B 1u21	CYP11B B1	C	G	R	R	cds	GE618	CTCCCAGTCA TTCCCTGA	GCCATGCTGC CCAGAC	CTCCCAGTCAATTCCCTGATccccctctgcacccgtcccgagacatlggtgcgctgttctctta ctctctgggtgcgaacccccgcttggctccagggcctgagcgtataaaccacagcgtggctag acatcaggggctcccgaggaaacttctaccagtgcccttggcttggcgtatgcccagcgtgctct ggcggc c g ctgagagagcagagatgctgctgctgcacatgtgagcagggcccgggc tggggaggggcctggcggggtCTGCGGAGCATGGGC	297
CYP11B 1u22	CYP11B B1	A	T	T	S	cds	GE625	GGAGGAGGCA GGAGGC	GTGTCCCTTCC CCATAGCAC	GGAGGAGGCAAGGAGGcctgggtgtgctcagcagtgcatctcccccgaagcagcaac ttgggtcttlttggagagcgggtggcctggttgcccaacagcccccaagttctggcagcctgaact tctctatgctcctggaggctca t tcaatccacccctccagctcatgttcatgcccagggcctg tctcgtgg a c c cagccccaggtgtggaagagcactttgagggcctgggaactgcatctcc agtaacgtgagggcagggacccccggcagGTGCTATGGGAAGGAGAC	307

FIG. 5N

[illegible]

FIG. 50

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
CYP11B 2d23	CYP11 B2	G	A	-	-	noncoding	GE533	ATCCAGCTGA GGACCCCTT	ACTGGGAGGG AGTTCTC	CATCCAGCTGAGGACCCCTTCTTg/a]tgatgccccccaccctccagggtcttaccctctggtgctcgt cttttgagcagtgatgagcttggtgtctcaagaactacacatccagctcgtgggtgag tgagcccccacacccctcgagctGAGAACCTCTCTCCCACTG
CYP11B 2d24	CYP11 B2	A	G	N	S	cds	GE587	ATGCTTTCCAG CACCAGAT	GGCATCACCCCT CTCTGGG	ATGCTTCCCAAGCACCAGATctgagggtctccctgctctctggacagggtgacaaactgtatcca gaaaactaccaggaaactggtctca]g]cgccctcaaacactacacagactctgfgcagag ctctctgtgagagggaaactgtcaactagaagccaataaagccaactctatgaaactcaactgcagg gagctggacacgggtcaggcagcaaccccccACAGAGGGGTGATGCC
CYP11B 2d25	CYP11 B2	A	C	R	R	cds	GE588	GAGTCTCTCTG TGCAAGTTC	CTCCAGCAGGG GGCCAG	GAGTCTCTCTCTGCAAGTcagacacctgagacgtctctg]agacagagctttcccttgcctga tgacgtcttttgagctggctcggaacccagcgtgagcagatctctggccaggagagcctggcc ggccagcagcagcatcagtgaaactccccagaaggaacaccagcagctgctgtgctggcggcgc ccctcaaggagaaacttg]a/c]ggtgggtgctggatgaggcctccctgtggcctCTGCCCCCTGCT GGAG
CYP11B 2d26	CYP11 B2	G	A	-	-	noncoding	GE610	CTGTGTCTCTG CTGTGGG	CAGGCTCTCTG GGCCTG	CTGTGTCTCTGCTGGGGgggctcacaaagctctgcccggcctctg]aggaatgggctcgaatgg cgcttcaaccgattgaggctgaacccagatg]gctgctcccaaggcctgagcagaggttctctccc gatgttgatgagtgagtgccaggagacttctccaggcctgagagaaggtgctgacagagccc gggggagcctgacccctggagcgtccagccagcatcttccactacacatagaaggtgtgggcat gggggaag]g/a]tccAGCCCCCAGAGACCTG
CYP11B 2u1	CYP11 B2	A	G	K	R	cds	GE610	CTGTGTCTCTG CTGTGGG	CAGGCTCTCTG GGCCTG	CTGTGTCTCTGCTGGGGggcctcacaaagctctgcccggcctctg]aggaatgggctcgaatgg cgcttcaaccgattgaggctgaacccagatg]gctgctcccaaggcctgagcagaggttctctccc gatgttgatgagtgagtgccaggagacttctccaggcctgala/a/g]agaagaaggtgctgcagac gctgggggagcctgaccttgagcgtccagcagcagcatcttccactacacatagaaggtgtggg ccatgagggaaggtctCAGCCCCCAGAGACCTG
CYP11B 2u10	CYP11 B2	G	T	R	R	cds	GE588	GAGTCTCTCTG TGCAAGTTC	CTCCAGCAGGG GGCCAG	GAGTCTCTCTGCTGGGGTcagacacctgagacatggctctctg]agacagcgtttcccttgcctga tgacgtctttgagctggctggacccagcgtgacagatctctggccaggagagcctggcc ggccagcagcatcagtgaaactccccagaaggaacccagcagctgctgtgctgag]g/t]g cgccctcaaggagaccttgagg]gggtgctggatgaggcctccctgtggccCTGACCCCCCTGCT GGAG
CYP11B 2u11	CYP11 B2	G	A	A	T	cds	GE637	TCCTGGGTGAG ATAAAGGATT	AGGATCTGGG TGTTCCC	TCCTGGGTGAGATAAAGGATTTgggctgaaacagggtggaggagcatggaaatggcactcagg caaaagcagaggtgtgctggcagcgcctgtgctctccctgcaaaaggcagggcactgggacact agagcc]g/a]ctcgggcccttagcaggtgtgcggttgaggcattccccagcactccagcga acaggtgtgctgaggtgctgcagatctggaggagacaggggtatgagcactgcactggagatg caccagaccttcaggagcgtggggccca]tttcagggtaaagcctctccctggcctcgtcgggaac ACCCAGATCCCT
CYP11B 2u12	CYP11 B2	G	A	P	P	cds	GE637	TCCTGGGTGAG ATAAAGGATT	AGGATCTGGG TGTTCCC	TCCTGGGTGAGATAAAGGATTTgggctgaaacagggtggaggagcatggaaatggcactcagg caaaagcagaggtgtgctggcagcgcctgtgctctccctgcaaaaggcagggcactgggacact agagccctcgggcccttagcaggtgtgc]g/a]cttgaggcattccccagcactccagcga acaggtgtgctgaggtgctgcagatctggaggagacaggggtatgagcactgcactggagatg caccagaccttcaggagcgtggggccca]tttcagggtaaagcctctccctggcctcgtcgggaac ACCCAGATCCCT
CYP11B 2u13	CYP11 B2	A	G	A	A	cds	GE587	ATGCTTCCAG CACCAGAT	GGCATCACCCCT CTCTGGG	ATGCTTCCCAAGCACCAGATcagagggtgtccctgctctctggacagggtgacaaactgtatcca gaaaactaccaggaaactggcctcaaccgctctcaaacactacacagcgtctggc]a/g]gag ctctctgttgaggaggaactgtcaactagaagccatcaaggcgaactctatggaactcaactgcagg gagcgtggacacggtcaggccagcaaccccccACCCAGAGGGGTGATGCC

FIG. 5P

[illegible]

FIG. 5Q

[illegible]

FIG. 5B

[illegible]

[illegible]

FIG. 5T

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
CYP21d	CYP21	C	T	P	L	cds	GE612	CTCTTGAGCTA TAAGTGGCACC	CTCTCTATGGT GAGGGC	CTCTTGAGCTATAAGTGGCACCtcaggccctgagccgctgctgcacatgctgcctctgggacctg ctgctgctgcccctgctggctgagccgctgctgaggaactgggaggaactccggagcct ccacttc/c/t gctcttgcctgggctcttgcaactgtgcgacgagcctcccaactat ctgcttggcctgactcagaacttggggcccatcacaggctccaccttgggctgcaaggtgagag gc/gatctcgctctgcccctcaccatAGAGG
CYP21d	CYP21	A	C	P	P	cds	GE612	CTCTTGAGCTA TAAGTGGCACC	CTCTCTATGGT GAGGGC	CTCTTGAGCTATAAGTGGCACCtcaggccctgagccgctgctgcacatgctgcctctgggacctg ctgctgctgcccctgctggctgagccgctgctgaggaactgggaggaactccggagcct ccacttcggcctcttgcgggggcttcttgcaactgtgcagccgacactcc/c a clatctat ctgcttggcctgactcagaacttggggcccatcacaggctccaccttgggctgcaaggtgagag gc/gatctcgctctgcccctcaccatAGAGG
CYP21d	CYP21	C	T	-	-	noncoding	GE629	TGTTGCCACTC TGACTCTCTCT C	GTTCCTGGAA GGAGCC	TGTTGCCACTCTGTACTCTCTccccaggccgcccgcac/c c / gctccttccacctctg caggagacctctctggcaggccctgagggagacatgagactacatgctccaaagggtggcgca ggcagcatggaaggcctctggacgctctggaagcagctggaagcagctgcacatgctgcagtgagcc tctgatcggtggcactgagaccacgacaacacctctctggcgcggttttttctgcttcac caccctgaggtgctgctggggagcaagcaaaGGCTCTCTCCAGCACC
CYP21u	CYP21	T	C	L	L	cds	GE612	CTCTTGAGCTA TAAGTGGCACC	CTCTCTATGGT GAGGGC	CTCTTGAGCTATAAGTGGCACCtcaggccctgagccgctgctgcacatgctgcctctgggacctg ctgctgctgcccctgctggctgagccgctgctggaactgggaggaactccggagcct ccacttcggcctcttgcggggcttcttgca/c c / gctgagccgacactcccaactat ctgcttggcctgactcagaacttggggcccatcacaggctccaccttgggctgcaaggtgagag gc/gatctcgctctgcccctcaccatAGAGG
CYP21u	CYP21	C	T	P	L	cds	GE629	TGTTGCCACTC TGACTCTCTCT C	GTTCCTGGAA GGAGCC	TGTTGCCACTCTGTACTCTCTccccaggccgcccgcacatgctccacctctcagg agacctctgaggcaggccctgagggagcatgagggacatgctccaaagggtggcgca/c /t /gacatggaagggctctggacgctctggaagcagctgacatgctgcagtgagcc tctgatcggtggcactgagaccacgacaacacctctctggcgcggttttttctgcttcac caccctgaggtgctgctggggagcaagcaaaGGCTCTCTCCAGCACC
CYP21u	CYP21	C	T	S	S	cds	GE544	CCGAGCCAGG GAGGTC	AGCCTCCACCA CATTTT	CCGAGCCAGGAGGTCctgcccagcctctaaactccagccctctcagcatctc/c t lggcac gacacctgaggggacagctacatctcgaacctcgaagccagccacactggaagagcgtctg ggagaggccacatgagttctggcctggatgtg/gggggggggggggcctggcgtgAAAATGCTGTG GAGGCT
CYP21u	CYP21	C	G	I	Q	cds	GE544	CCGAGCCAGG GAGGTC	AGCCTCCACCA CATTTT	CCGAGCCAGGAGGTCctgcccagcctctaaactccagccctctcagcatctcagca tccctgaggggcacagctacatctccgaacctccaagcgccca/c g tctgagtagcagcgtctg ggagaggccacatgagttctggcctggatgtg/gggggggggggggcctggcgtgAAAATGCTGTG GAGGCT
CYP21u	CYP21	G	A	A	T	cds	GE612	CTCTTGAGCTA TAAGTGGCACC	CTCTCTATGGT GAGGGC	CTCTTGAGCTATAAGTGGCACCtcaggccctgagccgctgctgcacatgctgcctctgggacctg ctgctgctgcccctgctggctggc/c a cccgctgctggaactgggagagctccgga ggctccacctccgctcttgcggggctcttgcaactgtgcgacgacactcccaactat ctgcttggcctgactcagaacttggggcccatcacaggctccaccttgggctgcaaggtgagag gc/gatctcgctctgcccctcaccatAGAGG
CYP21u	CYP21	C	T	-	-	noncoding	GE612	CTCTTGAGCTA TAAGTGGCACC	CTCTCTATGGT GAGGGC	CTCTTGAGCTATAAGTGGCACCtcaggccctgagccgctgctgcacatgctgcctctgggacctg cctgctgctgctgctgctggcctgaggtggggccgctgctggaactgggagagctccgga tctccacctccgctcttgcggggctcttgcaactgtgcgacgacactcccaactat ctgcttggcctgactcagaacttggggcccatcacaggctccaccttgggctgcaaggtgagag gc/gatctcgctctgcccctcaccatAGAGG

FIG. 5U

[illegible]

FIG. 5V

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
CYP21 ⁵	CYP21	A	G	N	S	cds	GE1208	CTGGCCTGGGTA TGTGGGG	AGGGAGGGGT TCGGTACAG	CTGGCCTGGTATCTGGGGGccgggggctgcgcgtgaaatgtggtgagactggtccccgcgtgc cgctgaacgctccccaccaccctgtccaccgccgcgcagatcgcttcttgagaccgggcaagaa ctccagactggtctcggtcgccgtgcgcgtgtgctggtggcgagcctgcggcgccctgg agctcttcgtggtgtgaacgcgactgctcagctgctgcgtgcgtgcgggacgcctg ccctccctgcagccctgccccactgcagtgatcctcaagatcgaccttccaagtcggct gcagcccggggagtgggggccacgccggggcagaa/g/cagatgatggcgaggaccgat gcagccgggtacactcagttctcttattgctcctCTACGAACCCCTCCCT
CYP21 ⁶	CYP21	G	A	R	K	cds	GE576	CTTTCATCATGTT CCCACCCTC	GGGGGCTACTG TGAGAGGC	CTTTCATCATGTTCCCAACCTTCagcccccacactcctcctgcagacaagctggtgtctat/g/a/gaa ctaccggactgtccttgggagactactcctgtcttggaaagccacagaagactcacccgt cagctcctgctcggaatccgtgtgagcagcagtggtggagcagctgacccaggagttc tgtgaggttaaggtctgggctcctgaggccactcgggtcagccttgcctCTCACAGTAGCCCCC
CYP21 ⁷	CYP21	T	A	I	N	cds	GE1225	CCACCTCGGGT CAGCCT	GCAGAAAGG AGGAGTA	CAACCTCGGGTCAAGCTTgcctctcagcagtagccgcgcctgcgcctgcacagcgctcgtg aactcaactgttctccacagcagcatgagacccagccagccctgtggccatcgagaggt aattctctctcctcaactgcagcatc/a/tgctgtactcactctggagacaaagatcaaggt gctctacagccctcagggccaccccccagccctcctcctgagcctctctctgtcctgaaactgaaag TACTCCCTCCCTTTCTGGC
CYP21 ⁸	CYP21	T	A	M	K	cds	GE537	GAGAGGCTCCT TCCCACA	CTGTGGCCGA GGGGAG	GAGAGGCTCCTTTCCACAGctgcatctcatgcttctcctgcgcagcttctccccaatccaaggtct cgagggtgaagcagcccatagagagagggatccatcgtgtgaga/t/a/gcagctgaggcag cacaaagtggggaactgtacgtggagggctCTCCCTCTGGCCACACAG
CYP21 ⁹	CYP21	C	G	L	L	cds	GE629	TGTTGCCACTC TGTACTCTCT C	GTTCCTGGGA GGAGCC	TGTTGCCACTCTGTACTCTCTCTccagccagcgcctcagccgcctcttctacccctctcaggt agagctt/c/g/gtgagcagccagtgagggagcatgatgactacatgctccaaggggtggcgca ggcgagcatggaaaggggctctgacagcctctggaaaggcagctgcatatggttgcagtgagcc tctgtgactggtgacactgagcacaacacctctcctctggggcggtgttttttgcctcac caccttgaggtgcgtctctggggaacagcaaaagcCTCTTCCTCCACAGC
DBH ¹	DBH	G	T	A	S	cds	GE991	CCCACACAGGC ATTTTTA	CGGCTACCT TCTATC	CCCACACAGGCATTTCATccacaggaagcagggcccttg/l/tccttcgggggtccagggctct ccagatctcctcgctggaagtgcactaccacacacactgg/tcATAGAGGTAGCGGC
DBH ²	DBH	C	T	K	C	cds	GE1034	CCCCACCAAGT TCNACA	GCAGCCACCT GGAAGC	CCCCACCAAGTTCAACACagagagatgtgtgcacctgcctcagggcgctgtctcagcagltca cctctgtctcctggaaactctcaac/t/gtggagactgagggcctctgacagctctcgcc catctccatgcactgcaaacagltcctcagccgtctccGTTCACAGTCCGCTGC
DBH ³	DBH	G	C	G	A	cds	GE1294	CAGTGTGGACC ACAGAGC	GCAGTGTCCC ATCGGT	CAGTGTGGACACAGAGGctcacccagcactgcgccctcagctgcgtggggcagcctgcgcgg ccagcatcgggaggcagccttcattgacagacagcagtgccctctctctgtcatctctgg ggccgactgcaggggtctgggtccccgtggagagccccctccctatccatccctggaccctg aggggtccctggagctctcatggaattcagctacacccagggggacatccattccagctctg gtcgaggggtc/aaggtcggtctgtttg/c/gtgcagcagcgtggcgagcttgagaaag cagatctgtgtgtctctggACGAGGGGACACTGC
DBH ⁴	DBH	T	C	V	A	cds	GE1034	CCCCACCAAGT TCAACA	GCAGCCACCT GGAGC	CCCCACCAAGTTCAACACagagagatgtgtgcacctgcctcagggcgctgtctcagcagltca cctctgt/t/c/tccctggaaactcctcaacgcagcagctgactgaagcctgtacagcttcgcgcc catctccatgcactgcacaagltcctcagccgtccGTTCACAGTCCGCTGC
DBH ⁵	DBH	C	G	A	A	cds	GE1034	CCCCACCAAGT TCAACA	GCAGCCACCT GGAAGC	CCCCACCAAGTTCAACACagagagatgtgtgcacctgcctcagggcgctgtctcagcagltca cctctgtccctggaaactcctcaacgcagcagctactgaaggtc/g/tgctacagcttcgcgc catctccatgcactgcacaagltcctcagccgtccGTTCACAGTCCGCTGC
DBH ⁶	DBH	G	A	T	T	cds	GE966	TTTCTCAGGG AGATGTG	CTTACCACTGT GGCCAGCTC	TTTCTCAGGGAGATGTGctcatcactcctctgcagctacaaac/g/a/gaagaccggagcctgg CCACAGTGGTAAG

FIG. 5W

[illegible]

FIG. 5X

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
DRD1u2	DRD1	C	T	Y	Y	cds	GE1170	GGATCTACAGG ATTGCTCAGAA AC	GCAATCTCCTC TAGCTTTTGG	GGATCTACAGGATTCCTCAGAAACAAATACAGCGCGCATTCGGCCCTGGAGAGGCGCAGCTCCAC GCCAAGAAATGCCAGAGCCACCAAGTAAGAGAGAGCTGCGAATGATCTCAACCGGAAAGTTC TTTAAAGATGCTCTCAAGAGAACTAAAGTCTCTGAAGACTCTGCGGTGATCATGGGTGTTG TTGTGTGCTGTTGGTCACTCTCTCATCTCTGAAGTGAATTTTGCCCTTTGGGTCTGGGAGG ACGAGCCCTCTGGCATGTGATTCACACCTTGACGTGTTGTTGGTGGTGGTGGTGAATTC ATCTTGAACCCCATCATTTAGCTTTAATGTGATTTTGGAGGCAATTTCAACCTCTTAG GATGTA [C/T] AGACTTTGCTCGACGAATATGCTAGAGACGAGTGAATATCAATAA TGGGCGCGGATGTTTCCAGCCATCATGAGCCAGAGCTCCATCTCCAAGAGTGAATCTGG TTTACTTGATCCCATGCTGTTGGTCTCTGGAGACCTGAAAGAGGAGGAGGAGCTGGCATC GCCAGACCTTGGAGAGGCTGCCAGCCCTATCGTCAATATGGACTATGACATGACCTGACGCTC CTGGAGAGATCCAACTCATCAAAACGCTGACCCCACTGACCTGAGTGAATCC TGCCACATGCTCATCCCAAAAGCTAGAGGAGATTC
DRD1u3	DRD1	C	G	V	V	cds	GE1173	CTGACCCCTAT TCCCTGCTT	CTCTCCAAAGC CGCAATG	CTGACCCCTATTCCTCTTAggaacttgagggtgtcagagccctgatgtgctttctctttagg aagatgaggactctgaacacctctccatggacgggactggctgtggtggagaggacttctc tgttgatctcactgactgtttctgtcgtgctcactctgtcagctctcagctctctgggaaacgc tggctgtgctgcgttatcaggttccgacacctgggtcccaaggtagcccaactcttttgcac tcttggctgtcagatctcttgggtcccttgggtcccttctgttaacatctgttggtcccttggacatcatgtgc agattgctggcttctggcccttgggtcccttctgttaacatctgttggtcccttggacatcatgtgc tccactgcacatcctcaacctctgtgtgacagctggagcaggtattgggtatctccagccc ttccgggtatgagagaaagatgaccccaagcagcctctcactcagtcagtgtggctatctccagcc tgtctgactcatctctctcactccagtcagctcagctggcacaagcgaacccacacagccc tctgatgaaatgccacttccctggctgagaccatagacaactgtgactccagctcagcaggac atatgccatctcactctgttaagctttacatccctgtgccaactgatgtccactaca ccaggatctacaggattgtctcagaacaaatcacggcgCATTCGGCCCTTGGAGAG
DRD1u4	DRD1	C	T	P	S	cds	GE1173	CTGACCCCTAT TCCCTGCTT	CTCTCCAAAGC CGCAATG	CTGACCCCTATTCCTCTTAggaacttgagggtgtcagagccctgatgtgctttctctttagg aagatgaggactctgaacacctctccatggacgggactggctgtggtggagaggacttctc tgttgatctcactgactgtttctgtcgtgctcactctgtcagctctcagctctctgggaaacgc tggctgtgctgcgttatcaggttccgacacctgggtcccaaggtagcccaactcttttgcac tcttggctgtcagatctcttgggtcccttgggtcccttctgttaacatctgttggtcccttggacatcatgtgc agattgctggcttctggcccttgggtcccttctgttaacatctgttggtcccttggacatcatgtgc tccactgcacatcctcaacctctgtgtgacagctggagcaggtattgggtatctccagccc ttccgggtatgagagaaagatgaccccaagcagcctctcactcagtcagtgtggctatctccagcc tgtctgactcatctctcactccagtcagctcagctggcacaagcgaacccacacagccc tctgatgaaatgccacttccctggctgagaccatagacaactgtgactccagctcagcaggac atatgccatctcactctgttaagctttacatccctgtgccaactgatgtccactaca ccaggatctacaggattgtctcagaacaaatcacggcgCATTCGGCCCTTGGAGAG

FIG. 5Y

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
DRD1u5	DRD1	A	C	A	A	cds	GE1173	CTGACCCCTAT TCCCTGCTT	CTCTCCAAGGC CGCAATG	CTGACCCCTATTCCCTGCTTAGgaacttgaggggtgtcagagcccttgatgtgcttctctcttagg aagatgaggactctgaacacctctgcacatggacgggaactgggctgggtgggtggagggagactctctc tggtctatctcactgctgtctctgtctgctgctcactctcctgcagcctctctggggaacacgc tggctgtgctgcgttatcagggttcgcagctcgggtccaaggtgcacaaactctcttgatc tcttgctgtcgaagatccttggtggcgctcttgatcctccctggagcgggtggttgagat tgctggctcttgacctctgggtcctcttgtaacatctgggtggcctcttgacatcatgtgctcca ctgc/a/c/tccatctcaacctctgtgtcagcgtgggacaggatctgggctatctccagccc tttcgggtatgagagaagatgaccccaaggcagcctctcatctgactgactggtggcctggaacct tgtctgactcatctctctcagctcagctcagctggcacaaggaaacccacaagacccc tgtatggaatgccactctcctggctgagaccatagacaactgtgactcagcctcagcaggac atatgccatctcatctctgttaagcttttacaatctctgtggccatcatgattgtcacctaca ccaggatctacaggattgtctgacaacaatacgggcgcatTTGCGCCCTTGAGAG	770
DRD1u6	DRD1	A	G	K	E	cds	GE1170	GGATCTACAGG ATTGCTCAGAA AC	GCAATCTCTC TAGCTTTTGG	GGATCTACAGGATTCTCAGAAACaaatccgcgcacttgccgctctggagggagcagcagctccac ggcaagaattgcagacacacacaggaatlaaggaaagcctgtcgaatgtctcacaacgggaagtctc tttaagatgtctctcaaaagagaactaaagctctcctgaagactctgctggtgctggtggtgtg ttgtgtgctgtggctaccttctctatctgaaactgcatcttgcctctctggtctctgggtgag acgcgacctcttgcatgattccaacacctttgacgtgtttgtggttttgggtgggctaaatc actctgaaacccatcatatgctcttaatgctgatttcggaaaggctcttcaacccctctag gatctacagactttgcctgcagcaatgacatgagtcagcgtgagtcagatcaatacaaatggg ggcgcgatgtttccagccatcatgagccacagagctccatctccaagagtgcaatcttggttta cctgatcccaatgctgtgggtcctctgaggacctgaaaggaggagggagcagctggcactgcga gaccttggaig/a/gtagctgccccagccctatggtcatattggactatgacactgacgtcttc tctggagaagatccaccctcatcacaaaaaggtcagcaccacaactgactcagatgaatctc tgccacacatgctcatcccaaaagctAGAGGAGATTGC	753
DRD1u7	DRD1	A	C	R	R	cds	GE1173	CTGACCCCTAT TCCCTGCTT	CTCTCCAAGGC CGCAATG	CTGACCCCTATTCCCTGCTTAGgaacttgaggggtgtcagagcccttgatgtgcttctctcttagg aagatgaggactctgaacacctctgcacatggacgggaactgggctgggtgggtggagggactctc tgttgatctcctcactgctgttctgtctgctgctcatctctgcagctctccagctctcgggaacacgc tggctgtgctgctgtatcagggtctcg/a/c/cactctgggtctcaaggtgacacaactcttctgt catctctggctgtgtcagatctcttggggcctgtggcgccttggtcaatggcctggagggcgtggctg agattgtggctcttggcctctctgttaaacatcgggtggcctttgacatcatctgtgc tccactgcatcctcatcactctgtgtatcagctggaacagatattgggctatctccagccc tttcgggtatgagagaagatgaccccaaggcagctctcatctgactgactggcattggcactgcc tgtctgactcatctctcctcagctgagctcagctggcacaaggcacaagcccaacacagacccc tctgatggaatgccactctcctggctggacacatgacaactgtgactcagctcctcagcagac atatgccatctcatctctgtlaaagcttttacaatctctgtggccatcatgattgtcacctaca ccaggatctacaggattgtctgacaacaatacgggcgcatTTGCGCCCTTGAGAG	770

FIG. 5Z

[illegible]

FIG. 5AA

[illegible]

FIG. 5BB

[illegible]

FIG. 5CC

[illegible]

FIG. 5DD

FIG. 5EE

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence	
DRD5u1 4	DRD5	C	T	A	A	cds	GE1171	CCAGGCAGCAA CGGCAC	CTGGCGCATGC GGTAGAT	CCAGGCAGCAACGGCACCGcgtaccgggggcagctcgctctataccagcagctggcgaggggaa cgcggtggggggtcggggggggaccccgccacgtggggcctccacaggtggtgacgcgctgcctgc tgacctactcatcatctggacctgctggaccctgctggcaacgtgctggtgtgctgcagccatcgtgggagc cgccacctgcgcgcacacatgaccaagctctcatcgctctctgggc[c/t]gtgtagaccttt tcgtggcgctgctggctatgccctgggaaggcagtcgcggaggtggcggttactggcccttggga gggtttctggagctctgggtggccttggacatcatgctccacctccctccatctgaacctgtg cgctacagctggagcgcctactggccatctccagggccttcggtacaaagcgaagatgactc agcgcatggccttggctatgctggcctggcagccttgcctcctcatctcttcatctcgg gtccagctcaactggcacaggacacagcgccctcttggggggggtggactgccaacaact ggccaactggagcgccttgggaaggagacttttgggagccagcgtgaatgcagagaactgtgact ccagcctgaatcgaaactacgccaatctctctctgctcatcagcttctacatcccgttgccttc atgatcgtaactacacgcgcgtATCTACCGCATGCCGACG	754
DRD5u1 5	DRD5	T	G	L	R	cds	GE1171	CCAGGCAGCAA CGGCAC	CTGGCGCATGC GGTAGAT	CCAGGCAGCAACGGCACCGcgtaccgggggcagctcgctctataccagcagctggcgaggggaa cgcggtggggggtcggggggggaccccgccacgtggggcctccacaggtggtgacgcgctgcctgc tgacctactcatcatctggacctgctggaccctgctggcaacgtgctggtgtgctgcagccatcgtgggagc cgccacctgcgcgcacacatgaccaagctctcatcgctctctgggc[t/g]tt tcgtggcgctgctggctatgcccttgggaaggcagtcgcggaggtggcggttactggcccttggga gggtttctggagctctgggtggccttggacatcatgctccacctccctccatctgaacctgtg cgcttctgagcgtctgggtggccttgcacatcatgctcctcactgcctcctgaacctgtg cgctacagctggagcgcctactggggccatctccagggccttcggtacaaagcgaagatgactc agcgcatggccttggctatgctggcctggcagccttgcctcctcatctcttcatctcgg gtccagctcaactggcacaggacacagcgccctcttggggggggtggactgccaacaact ggccaactggagcgccttgggaaggagacttttgggagccagcgtgaatgcagagaactgtgact ccagcctgaatcgaaactacgccaatctctctctgctcatcagcttctacatcccgttgccttc atgatcgtaactacacgcgcgtATCTACCGCATGCCGACG	754
DRD5u1 6	DRD5	T	C	T	T	cds	GE1171	CCAGGCAGCAA CGGCAC	CTGGCGCATGC GGTAGAT	CCAGGCAGCAACGGCACCGcgtaccgggggcagctcgctctataccagcagctggcgaggggaa cgcggtggggggtcggggggggaccccgccacgtggggcctccacaggtggtgacgcgctgcctgc tgacctactcatcatctggacctgctggaccctgctggcaacgtgctggtgtgctgcagccatcgtgggagc cgccacctgcgcgcacacatgaccaagctcttcatcgctctctgggc[t/g]tgcagacctttcgt ggcgctgctgctgctatgcccttgggaaggcagtcgcggaggtggcggttactggcccttggga tcgtgagcgttgggtggccttggacatcatgctccacctccctccatctgaacctgtg cgctacagctggagcgcctactggggccatctccagggccttcggtacaaagcgaagatgactc agcgcatggccttggctatgctggcctggcagccttgcctcctcatctcttcatctcgg gtccagctcaactggcacaggacacagcgccctcttggggggggtggactgccaacaact ggccaactggagcgccttgggaaggagacttttgggagccagcgtgaatgcagagaactgtgact ccagcctgaatcgaaactacgccaatctctctctgctcatcagcttctacatcccgttgccttc atgatcgtaactacacgcgcgtATCTACCGCATGCCGACG	754

FIG. 5FF

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
DRD5ul17	DRD5	T	G	V	V	cds	GE1171	CCAGCGACGAA CGGCAC	CTGGCGCATGC GGTAGAT	CCAGCGACGAAACGGCACccgcgtaccgcggggcagttctgcctctataccacgagctggcgcaggggaa cgccgtggggggctcgggggggcacgcgcacccgggcccctcacagtggtgccacgcctgcctgc tgacctctcatcatctggacctgctgggaacgctgctgggaacgctggtgtgtgcacgacatctgcggagc cgccacctggcgcacacatgacacacgtctcatctgtctctggcccttcagagccttttcgt ggcgtgtggtcatgcccctggaaggacgctccgagatggccggttaactggccctttggagcgt tctgcgagcttgggtggccttgacatcatgtgctccactctccatctccactgccttgcgctc atcagcgtggaccgctactcaggccatctccagcccttcgctcaagcgaagatgactcagcg catgaccttggtcatgttcggctggcatggacctgtccactctcatctctcaatccgctcc agctcaactggcaccaggaccggccctcttggggggggcttgggacctgcctcccaaacctggcc aactggacccctgggaggaggacctttgggagcccgagtgaaatgcagagaaatgtgactccag ctgaaatcgaaactacgcacatctctctctgctcatcagctttacatcccgttt/g/gjccatc atgactgtgacctacacgcgATCTACGCCATGCCACG
DRD5ul18	DRD5	T	C	L	L	cds	GE1171	CCAGCGACGAA CGGCAC	CTGGCGCATGC GGTAGAT	CCAGCGACGAAACGGCACccgcgtaccgcggggcagttctgcctctataccacgagctggcgcaggggaa cgccgtggggggctcgggggggcacgcgcacccgggcccctcacagtggtgccacgcctgcctgc tgacctctcatcatctggacctgctgggaacgctggtgtgtgcacgacatctgcggagc cgccacctggcgcacacatgacacacgtctcatctgtctctggccgtgcagaccttt/g/l tctgtggcgtgctggtcatgcccctggaaggacgctccgaggtggccggttactggcccttggga ggcttctgcgacttgggtggccttgacatcatgtgctccactctccatctccactgaactctg cgctacagcgtggacgctactggccgctctccaggcccttcgctcaagcgaagatgactc agcgcattggccttgggtcatgttcggcctggcatggaccttgtccactctcatctctccatccg gtccagctcaactggcacaggacaggcgcccttttggggggctggagctccctcccaaacact ggccaaactggaccgctggaggaggacctttgggagcccgacgtgaaatgcagagaaatgtgact ccagcctgaaatcgaaactacgcacatctctctctgctcatcagctttctacatcccgttgcac atgactgtgacctacacgcgATCTACGCCATGCCACG
DRD5ul19	DRD5	G	A	G	E	cds	GE1171	CCAGCGACGAA CGGCAC	CTGGCGCATGC GGTAGAT	CCAGCGACGAAACGGCACccgcgtaccgcggggcagttctgcctctataccacgagctggcgcaggggaa cgccgtggggggctcgggggggcacgcgcacccgggcccctcacagtggtgccacgcctgcctgc tgacctctcatcatctggacctgctgggaacgctgctgggaacgctggtgtgtgcacgacatctgcggagc cgccacctggcgcacacatgacacacgtctcatctgtctctggcccttcagagccttttcgt ggcgtgtggtcatgcccctggaaggacgctccgagatggccggttaactggccctttg/l/a ggcttctgcgacttgggtggccttgacatcatgtgctccactctccatctccactgaactctg cgctacagcgtggacgctactggccgctctccaggcccttcgctcaagcgaagatgactc agcgcattggccttgggtcatgttcggcctggcatggaccttgtccactctcatctctccatccg gtccagctcaactggcacaggacaggcgcccttttgggagcccgagtgaaatgcagagaaatgtgact ggccaaactggaccgctggaggaggacctttgggagcccgacgtgaaatgcagagaaatgtgact ccagcctgaaatcgaaactacgcacatctctctctgctcatcagctttctacatcccgttgcac atgactgtgacctacacgcgATCTACGCCATGCCACG

FIG. 5GG

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
DRD5u2	DRD5	G	C	S	C	cds	GE1171	CCAGCGACGAA CGGCAC	CTGGCGCATGC GCTAGAT	CCAGCGACGAAACGCGACCGcgTaccctggggcaggttgcctctataccagcagctggcgaggggaa cgccgtggggggctcggcggggacgcgcacatggggccctcacaggtggctacccgctgctgcg tgacctactcatcatctggaccctctgggcaacgctgggtgg/gc/cgcagccactgctgcg ggaccgcaactcgcgcgcaacatgaccaacgtctctatcgtgtctctggcgctgtccaaaccttt tcattggcgctgcggctatgcctgggaaggcagtcgcggaggggggcttactggcctcttggga gggtttctggagctgggtgggcttcgacatcatgtctccactgtccactctccatctccatggacccgtg cgctacagctggagccctactggccctctccaggcctctccgctacagagcaagatggactc agcgaatggcttggctatggctggcctggcctggacatgtctcatctctcatctctcatctcg gtccagctcaactggcaaggaccagggcctcttggggcgggctggaccttgcgaacaaacct ggccactggagccctgggaaggagacttttgggaagccgagctgaaatgcagagaaactgtaact cgaagctgaaatcgaaactacgccatctctctcgtctcatcgaagcttctacatccccgttgcac atgactggactcacgc/ga/cTACCGCATGCCACG
DRD5u2 0	DRD5	G	A	R	H	cds	GE1171	CCAGCGACGAA CGGCAC	CTGGCGCATGC GCTAGAT	CCAGCGACGAAACGCGACCGcgTaccctggggcaggttgcctctataccagcagctggcgaggggaa cgccgtggggggctcggcggggacgcgcacatggggccctcacaggtggctacccgctgctgcg tgacctactcatcatctggaccctctgggcaacgctgggtgg/gc/cgcagccactgctgcg ggaccgcaactcgcgcgcaacatgaccaacgtctctatcgtgtctctggcgctgtccaaaccttt tcattggcgctgcggctatgcctgggaaggcagtcgcggaggggggcttactggcctcttggga gggtttctggagctgggtgggcttcgacatcatgtctccactgtccactctccatctctcatctcg ctctggagctctgggtggcttgcacatcatgtctcactgactctcatctgaactctggactc atcagctggagcctactggcctaccagccctctccgtacagcgcaagatgactcagcgt catggccttggatcatggctggcctggcagcttggcctcatctcatctctcatctctcgtgctcc agctcaactggcacagggaccagggcctcttggggcgggctggacctggcaaacacctggcc aactggagccctgggaaggagacttttgggaagccgagctgaaatgcagagaaacttggactccag cctgaaatcgaaactacgccatctctctcgtctcatcgaagcttctacatccccgttgcacatcga tcgtgactcacgc/ga/cTACCGCATGCCACG
DRD5u3	DRD5	C	G	N	K	cds	GE1171	CCAGCGACGAA CGGCAC	CTGGCGCATGC GCTAGAT	CCAGCGACGAAACGCGACCGcgTaccctggggcaggttgcctctataccagcagctggcgaggggaa cgccgtggggggctcggcggggacgcgcacatggggccctcacaggtggctacccgctgctgcg tgacctactcatcatctggaccctctgggcaacgcttgggtgg/gc/cgcagccactgctgcg cgccacctcgcgcgcaac/c/g/atgacaaagcttctcatctctctggcgctgtcagacactt tcgtggcgctcgtggtcatgccctggaaggcagctggcgaagtgccgttactggcctcttggga gggtttctggagctgggtgggcttcgacatcatgtctccactgtccctcgtcctacacgaactg cgtcatcagctggagcagctactggggccctctccagccctctccgtctacagcgcaagatgactc agcgaatggccttgggtcatggctggcctggacttggacttctcatctctcatctctcatctcg gtccagctcaactggcacagaccagggcctcttggggcgggctggacctggcaaacacct ggccaaactggagccctgggaaggagacttttgggaagccgacgtgaaatgcagagaaacttggact ccagcttgaatcgaaactacgccatctctctcgtctcatcgaagcttctacatccccgttgcac atgactggactcacgcgca/cTACCGCATGCCACG

FIG. 5HH

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
F10d8	F10	C	T	F	F	cds	GE942	GGTTTTCAGTC AGGCAACAC	CAGACAGTGAC GGTGCCC	GGTTTTCAGTCAGGCAACACNagtcacactggccagccacactgagcctgtcacgtctgtgtcacag gccccgtctatcaatgaggaagaaacagaggtttctgtgtgtgaacattctgagcgagttctacat cttaacggcagccactgtctctaccaagccaagagatttc/l gaaagtgaggttaggttaagt accaacagccccagggcgtggtgggggggacacggtCACGTCTCTG
F10u1	F10	C	T	T	T	cds	GE942	GGTTTTCAGTC AGGCAACAC	CAGACAGTGAC GGTGCCC	GGTTTTCAGTCAGGCAACACNagtcacactggccagccacactgagcctgtcacgtctgtcacag gccccgtctatcaatgaggaagaaacagaggtttctgtgtgtgaac/l t tctctgagcgagttct acatcttaacggcagccactgtctctaccaagccaagagatttcgaaggtgaggttaggttaagt accaacagccccagggcgtggtgggggggacacggtCACGTCTCTCTG
F10u2	F10	A	T	E	V	cds	GE907	GTCCCTGGCT GACCTG	GTGGATCTCA CTTTAATGG	GTCCCTGGCTGAGCTGAGcagagtcacactcgctgtctcccgggagcgggaacacggagcagga ggagggcgtgagggcgtgtgacg/l t ggtgaggtgtgtcatcaagcacaacacgggttcacaag gagactatgactctgacatcgccgtgtctccgtctcaagaccctcatcacttcgcgtacagct ggcctgtcctctcccagcggtgactggcggaagtcacgctgagcagcagagagcggga ttgtgagggcttcggcgccacccagagagggccggcagctccacaggtccaagatgctgag gtgctctacgtgagccgcaacagctgcaagctgtccagcagcttcacatccacagaaatgtt ctgtgcccgtacgacacacagcagagagatgctgacagagctgtcagctgggagaggtgtgcccgtca ccgcttcaggacacactacttctgacagagctgtcagctgggagaggtgtgcccgtcaag gggaagtcagggatctacacaggtcacgcctctctcaagtggtgacaggttccatgaaac caggggttgcaccaagccaagcctgccccggaggtcataacgtctctCCATTAAAGTGAG ATCCAC
F10u3	F10	C	T	A	A	cds	GE907	GTCCCTGGCT GACCTG	GTGGATCTCA CTTTAATGG	GTCCCTGGCTGAGCTGAGcagagtcacactcgctgtctcccgggagcgggaacacggagcagga ggagggcgtgagggcgtgtgacg/l t ggtgaggtgtgtcatcaagcacaacacgggttcacaag cctatgactctgacatcgccgtgtctccgtctcaagaccctcatcacttcgcgtacagct ctgctctctcccagcggtgactggcggaagtcacgctgagcagcagagagcggatgt gagcgtctcggcgccacccagcagagggcggcagctccacaggtccaagatgctgaggtgc cttaagtgagccgcaacagctgcaagctgtccagcagcttcacatccacagaaatgttctgt gc/l t ggctacgacacacagcagagagatgctgacaggtggcgggagcagggggccgcagctca ccgcttcaggacacactacttctgacagagctgtcagctgggagaggtgtgcccgtcaag gggaagtcagggatctacacaggtcacgcctctctcaagtggtgacaggttccatgaaac caggggttgcaccaagccaagcctgccccggaggtcataacgtctctCCATTAAAGTGAG ATCCAC
F10u4	F10	G	C	Q	H	cds	GE250	CCTGCCCTTCA GTGTTCAT	CCGAGCCCTTA CCGTCTTG	CCTGCCCTTCCAGTCTTATccgagagagca/l c lgccaaacacatcctggcgaggggtcacgag ggccaatctcttctgagagatgagaaagacacactcgaaagagagtgcatggaagagacct gtccatagcaagaggcccgagggtcttggagcagcgaCAAGACCGTAAAGGCTTGG
F10u5	F10	C	T	N	N	cds	GE913	GAGCCTGGCTT CTGGCTA	CGTGCCTCTTA CCGTGTG	GAGCCTGGCTTCTGGCTATAaacgcgcactgcacatgagcttccccgtgacccgtgaggttgcgc tcaagggcaagtgcactgcctgcctgtgccttctgctcaacccatggcgcttctgtgc tgacagggcaagtggatgagctggcacccttggccagccagcctcctctctccagctgtcc cagagccaacgtgctctctcttctggcagtcacacggagagctctgcagctggacaa/l c t gggg actgtgaccagtctctgcacaggggaacagaaactgtgggtgtctctgctgcccgcgggtacac ctggctgacaacggcgaagggcctgcatccCACAGGTAGGACGACG
F10u6	F10	C	A	L	I	cds	GE242	AGCCAGACAA AGCCATCC	GGCAGGGGAC TTACGACT	AGCCAGACAAAGCCATTCcagctgggggtgagacttctctcagcagcctgtcccagtgagggac agggacacagtaactcggccacacactggggcgccctcctgcac/l a t cgtctgtcagtgct ccctggcgtgctctctgctgctggggaaAGTGTAAAGTGTCCCTTCCG

FIG. 5KK

[illegible]

FIG. 5LL

[illegible]

FIG. 5MM

45/178

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
F11u3	F11	A	G	T	T	cds	GE287	TGACTTTACTTT TCTCTAGGTC TG	ACCCTCCCTCA GCATGTATC	TTGACTTTACTTTCTCTAGGTCCTGCAAAATGTTTCTGTTGATGATATATTTCTACTT cccttttggtttggtagaatacttctctctcaacatctcgagagtgatggccagatc /g/cgcattaaaagagcaaaagctcttctgggttcagctctcaaaagctcgagccacagatcccc aggtaaactgagagttctgcatctggctgagagtgaccagcccgagggagccgATACATGCTG AGGAGGGGT
F11u4	F11	A	T	II	I	cds	GE916	TGGAAGGAG ATGTAGGAGC	GCAATAAGAC AATCTAATGG TTAAAGTA	TGGAAGGAGAGATGTAGGAGCTGCTCATCATCAATGCTTCTGTCGAGAGTGTACCCCAAAATC agggccaggatcggtggaggaactctgctgggtgggagtgccgagtgccgagtgccgagtgccctgca cacaacctcaccctcagagcacactgtgtggagctccatcttgaaacccagtgagataltaa cagccgtc/a/tjctgttctatgggtcagtcaccagcggtttttatagttcatcttctca cacatttataaaaaatattactagcatgttaggaataaatCTTTAACCAATTTAGATTGCTTTA TTTGC
F11u5	F11	A	T	I	F	cds	GE339	GCCACACACTT CACAAATGTC	CAGGCCGTAG TCTAGTAGTGT TAAA	GCACACACTTTCACAAATGCTCTGGGAATTTTtagtaaaagaaattcttctccctctgtgtgt gctcttaggttagagtcactgaagattttgctgctcactagtggaatctttaaataatctgtaa taaaagggacacatcttcttgggtttcaagaataataatccatgatcatgataaaatggca gaagcggtatgat/a/tjctgcttggtaactgaaacccagtcgaattacacaggtacgg agaatttctccggaaagtgtctccaatgggaactggataaaatgTTAACACTACTAGACTT ACGGCTCG
F11u6	F11	A	F	E	V	cds	GE324	CCTTTATGAGA TTACCACCTAA CTAGA	TTTAAAATCT GTCCTCTCGAT GT	CCTTTATGAGATTACCACTTAAGTATGATGCCAGTAAATCCAACTAACCGCATCGATGT actacatcacag/a/tjctgtgactcagttgttgaggacacctgcttgaaggaggaggacat tactacggtcttcacacccagcccaagtcagtcagtgagtcgactaccacccaagatgtt tactcttcacttccagcgcggaatcacatctgaagtccccaccgagtgtaaatgcttatgttt ctACATCGAGGAGACAGATTTTAAA
F11u7	F11	C	T	D	D	cds	GE283	GTATTGTGTAT GGTTATTCTAC AAACG	AAAACCCCAA GCATTTAAG	GTATTGTGTATGTATTCTTACAAACGcaaaaaatttttccagacaaaaatacaaaatact ctccagaagaacccagaTacccttagtgaccacacagagagtgccagagagatcacagagacataa aataacccataaagatgatctgtgccggtcacaggaagaggaggagga[c/t]gcttgcaaggta acagagtggtcttagcccaatgggaatataTgcaaatgggaatgCTTAAATGCTGGGTTTTT
F11u8	F11	G	A	E	E	cds	GE352	TGAGCAAGATG TGCTGAAGAT	AGCAVGCTGG ACAGTGAA	TGAGCAAGATGCTGTAAGATGggagagcgtctgagtgtatctgtgacaccttcttctgtccct cgttctaggagatctggggagccctctgctgcaacacaaatagagtcgcatctgtgagggc atccagagctggggcgagggctgtgtctcaaaagcggccaggtgtttacacacagtggtcga /g/a]tgcgtggactgattctggagaacactcaagcagtgatgaatgggttccaggggcccattg gagtcctctgaagaccacaggaatttgcgtggagaggggttgagTTCACTGTCGAGCATGCT
F11u9	F11	T	C	I	P	cds	GE324	CCTTTATGAGA TTACCACCTAA CTAGA	TTTAAAATCT GTCCTCTCGAT GT	CCTTTATGAGATTACCACTTAAGTATGATGCCAGTAAATCCAACTAACCGCATCGATGT actacatcacagaatgtgtgactcagttgttgaggacacctgcttgaaggaggaggacattact acggtcttcacacccagcccaagtcactgcccaggtagtcgactaccacccaagatgttctc t/c]tctcaacttccagcgcggaatcacatctgaggatccccaccgagtggttaaatgcttatgttt ctACATCGAGGAGACAGATTTTAAA
F13A1d 24	F13A1	C	T	-	-	noncoding	GE284	TGCCATGAATC TTGCAATATC	CAACTTTTACG TTACTCTTTCA TGTC	TGCCATGAATCTTCAGTATCTGggacagaattggagatgacaaactcac[a/c]tgcccttctc ctgtgcaatgcaggatgatcggtgtggccctcctgttcaagcctcaacagcagcgccatgt ctgcttccaatttgatgcacctttgttttctgagagagcagcagagagcgtggaggaagtgctg tttcttccccaacctcttaacACATGGAAGAGTAAAGTTG
F13A1d 25	F13A1	T	C	-	-	noncoding	GE284	TGCCATGAATC TTGCAATATC	CAACTTTTACG TTACTCTTTCA TGTC	TGCCATGAATCTTCAGTATCTGggacagaattggagatgacaaactcac[a/c]tgcccttctc ctgtgcaatgcaggatgatcggtgtggccctcctcgttcaagcctcaacagcagcgccatgt ctgcttccaatttgatgcacctttgttttgcagagtagcaggaagcgtggaagagtgctg tttttcccccaacctcttaacACATGGAAGAGTAAAGTTG

FIG. 5NN

[illegible]

FIG. 500

[illegible]

FIG. 5PP

[illegible]

FIG. 5QQ

[illegible]

FIG. 5RR

[illegible]

FIG. 5SS

[illegible]

FIG. 5TT

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
F13Bu1 6	F13B	T	C	P	P	cds	GE370	CTTGAGAAGC TTTGCTAAAT G	GGCTTAACAGT GGCTTTTCTCT A	CTTGAGAAGCTTTGCTAAATGaaatctgcgtgtagctaaatggtcagttctcttccaactg tacctttcagaagacagagagagctgctgtaggaacaccccttcagatgaaatgylgcag caaatctacactcaagatttatacaatggggaataaagtacatctgctgaaatgagctac cttctccatgagatgaaatgaaatctgtaactgtaactggaatggaacactcc [c] cctgagt gtcttggtgatgctacatttaccatcagtagctaaacttattgggtgtaaaattttccactctg ttacttaactggaatattccttAGGAANAGACCACTGCTTAGCC
F13Bu1 7	F13B	T	A	N	K	cds	GE400	TTTGCTGTCAA CTCTTGCTTAG	AAATGAGAGAG AAACACATTGT GAAA	TTTGCTGTCAACTTTCCTTAGCaaattttaaataatttgagctgaaataatttttcataattg taatgaattataaacaacttgcctcaatataatacaataactcagacactatgatatgag ttactatgatatattgtatgagctcatataattttaaacaacctctttcttagaataa [c/a] /aattgagaattgtaagcactcctctgtgtgaatgagtggtctgttcgaacgggacttggcaa gctatgaacaggactcctcagtggaatataagatgcaatgaatatctactcaggggatacaaaa atactcgttgcgaacaaggaaatggtcatcccacctgtttgtcttgggtgagaagaagacac atggaatgctacgtttgtactttatgttttctacagtgttttatcatcatgaaaaatgatg attttgacaaatctttttTCACAAGCTTTTTCCTCTCTCATTT
F13Bu1 8	F13B	G	C	L	L	cds	GE264	AAATTTGAAG GCTGAGATTGT AA	CAATATTTAA GCAAGGAAAA CTCC	AAATTTGAAGGCTGAGATTGTAattaaacactgactcgaattgatcttatttcaaaaactct cttttccctcaagcaact [c/g/c] tcttatacagaacaccttaagaacatagaaatgaatggca gaaagaggtcatatttcaatacatcatgaaattcctataaaataaattttggggaataaag ttaaasacttCGAGTTTTTCTCTGCTTAATTTTG
F13Bu1 9	F13B	T	A	N	K	cds	GE400	TTTGCTGTCAA CTCTTGCTTAG	AAATGAGAGAG AAACACATTGT GAAA	TTTGCTGTCAACTTTCCTTAGCaaattttaaataatttgagctgaaataatttttcataattg taatgaattataaacaacttgcctcaatataatacaataactcagacactatgatatgag ttactatgatatattgtatgagctcatataattttaaacaacctctttcttagaataa [c] t/a] ggaattgtaagcactcctctgtgtgaatgagtggtctgttcgaacgggacttggcaa gctatgaacaggactcctcagtggaatataagatgcaatgaatatctactcaggggatacaaaa atactcgttgcgaacaaggaaatggtcatcccacctgtttgtcttgggtgagaagaagacac atggaatgctacgtttgtactttatgttttctacagtgttttatcatcatgaaaaatgatg attttgacaaatctttttTCACAAGCTTTTTCCTCTCTCATTT
F13Bu2	F13B	A	G	M	V	cds	GE396	TGTTTGATGTT TAAAGTCATT GC	CATTTTATG GACCCCTATT T	TGTTTGATGTTTAAAGTCATTTCagatcaattatgataaaggactccttgagttgtcacaaa gtacctaaaataattgaaglaaqaataaagtaactagttgagtgctctcaaaaacttttagttt gtattgtcactgattacaaaattttagtttttagattgttttccatactcagcttgacattta ctcatttcagaacaacctgtgttttctcatgtggaataatggaataatgccaataattacta tactttaaaagcttttacttcca [a/g]tgagcatagacaaaattgtcatttttctgcttg gctgggtataccactgaagtggagacaagaagcaccgtgtacacaagaagcgtggct tccagggcagggtgcttcagtcagtcagtggaatgtcactcaatgtttcactcaactcaagaa atttgtataAAATTAGGGTCCCAATAAAATG
F13Bu3	F13B	A	G	H	R	cds	GE373	CCAATGMAA TCGCCAATAAT A	TTCTCTGATTG TAGACATAATG A	CCAAATGMAATGCCAATAATATATcatctactttttggcttaatttcaaatcttagtaaaagaca agcttagtttcatatgaatttaataatttttttcccatagataaaatgcactaagctgacct gagtaattggtacactctcgtgataaagttattgtataaaattcaagagaaatgc [a/g] ttat gggtgcgcttcagggtacaaaacctcaggaggagatgaagaagggttccatgctctctga tggatgggtcttctcaaccaacctgtggaagaacatggtataagaattcttccaaancctga gataagtgctctcaagcttatattggaatatattggaagcttatctgatactatttatttgaatg aatttattttTCATTATGTTTCAATGTCAGCA

FIG. 5UU

[illegible]

FIG. 5VV

[illegible]

FIG. 5XX

[illegible]

FIG. 5YY

[illegible]

FIG. 5ZZ

[illegible]

FIG. 5AAA

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
F5u26	P5	C	T	-	-	noncoding	GE924	TTGCTGTGCGCT AAACTCTTTG	GAAGACGACG CGAATAATTAC TA	TTGCTGTGCGCTTAACCTCTTTGCTGtataatccaggaagaagttaagagtgcttttattctgcagagtgctactgaaacaagctcttctctcattagggccctaaactgaggggaggaagacagagcgttgagacagcaaatcgctctactattgtgtgttgagaaagagagctggagccagctcatcatccctaatccacagctcaatggatgtgaaatggacaacatgccaggttaaca c/t gagggctgltgaccatTaaacaacagtaaaatcatTAGTAAATTTCGTGCTCTCTTTTC
F5u27	P5	A	G	E	E	cds	GE494	TCTGTCTCTCT TCTGTAGGAAC T	CCCTGTGACAT CTGGCTGTAG	TCTGTCTCTTCTTAGAGTgtaactctccatgaattctagctccaagaagcaaaaagctggagctgaattctcagagatgtaaatcatccagatgatgcagatgcagatgcagatgcagatggtgaacctcagaatctacagctcattggctacacggaaatgcgatcggtttagaacctcgaagatggagagtgatgctgactgattcaccagaacagctggctgcagctcaggaatctaggatctaggctatccgaaactcatctgaaacgaagaagaagatgtaacttactgcctagctcagctcggagaatgcactga a/g t tgcgttcttcgaacagatataattgttgttcaaat attcttccccaaagttaat tagtaagttcaactgcaacttgacaacctcagaagcccttctcaccacaagccaccacagctgttccccactgagacactctatggcaagaacactcagttctcattcttctccacagcagagatctccagcccatctctgagagccctatagaggtctctCTACACCTAGATGTACAGGG
F5u28	P5	C	T	S	S	cds	GE391	CCCTCTCTCAC CACAAAGC	AGCACGTGAGG CATTTCTGG	CCCTCTCTCACCAACGacacacagctgggttccccactgagacactcatctggcaagaagatcgttctcaattctccacagcaggtctccag c/t ccatattctgcagactcatctatggagactacctctacagccagatgtcacaggtatcgtctacttctacttggctgggagatctagaagcttcctggaaactgaagctaaagggcccaaggttagaagacatcaagcagcaacagcacaggttctctcagatgaaattactagcacataaagttggagacacctaagccaagacactggttctctctccggaa tgaggccctgggaggaaccttctagcccaagacactgggttctctctcaggaatgagccctgggagggacctctctagtgatgttactcttaaaacaagtaactcatctagatgttgggttgggagatggcttggctcttgagaaaggtagctatgaaataatccagaatactgatgagacacagctgttaacaattcggctgatcagcccccCAGAAATGCCCTACGTCCT
F5u29	P5	A	T	K	*	cds	GE389	GAAGGTAGCT ATGAATAATC CAAGA	GGGTCTGAAAT GGGGAATGT	GAAGGTAGCTATGAATAATCCAAAGAtactgtagaagacacagctgttaacaattggctgatcagccccagaatccctcagctgcttggggaagaacactctctgccacaacactgggaagcagagtgagtgccacccaaggttctctcagagtttagacataaaatctctcaagtaagacaggttggaggaagagtagtagactgaagaaagccaggttctctatgaagacagcaaaaaaagaagaagacacacacacctgctcttatactccggagcccttccaccttaagaagtgagctcacaacacttcttca gaaagaagacttaagcatctgtgtgtgtctcat a/t aatccaatgaacactctcttctccacagacctcaatcagacattgccctctatggatttgggtgtagctcactcctctgaccataatcagaaattctctcaaatgacactggtcaggaagctgtctctccaggtctttatcagacagtgcccccaaggaaactatcaaaCTCCCTCTCAAGACC
F5u3	P5	G	A	R	Q	cds	GE47	GAATAACTTT GCAATGAAA CA	TTTCTGAAGG TTTACTCAAGG AC	GAATAACTTTGCAATGCAAAACAAatttgaatataatttctctcaggcaggacaacacatgactcagagcaggttcaaccagggggaacctataactataatgaggaaacatttagagtttgatgaacccacagaaaaatgatccccagtgcttaacagaccatactacagtgacgtggacatactagagacatcgctctctgggtcaataggaactacttcaattctgttagagcagatccctggacaggtc g/a aggaatacaagctatttCTCTTGAAGTAACCTTTCAGAA

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Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
F5u30	F5	C	A	P	T	cds	GE989	GAAAGTAGCT ATCAAAATATC CAAGA	GGGTCTTGAAT GGGAATGT	GAAAGTAGCTATGAATATCCAAAGATactgatgaagacacagctgttaacaattggctgatca gccccagaaatgcctccacgtgcttggggagaaagaccctcttggccaaagccttggaagcag agtggccaccacaaagtctctcagagtagataaaactctcaagtagaagacagctggagga gagtagctgaagaaagccaggttctctattgaagacacaaagaaagaaagagagacacac acctgctcttctcagagaccttccacctcaagagtagaagctacacacatttca gaagaagacttaagcattctgttggtcttcaaatcaatgaacacatctctccacagacct caatcagacattgcccctcctaggtatttggctggatagctcactt(c/a)ctgacataatcag aatctctcaatgacactggcagcagctgctccaggtcttctatcagacagtgccccaga ggacacactatcaacATTCCTCCATTCAGACCC
F5u31	F5	G	A	M	I	cds	GE925	CACCTGCCCTC TCTGTGTC	CAGATTGCCCTT TTCCTGTATT	CACCTGCCCTCTCTGTGTGTCaagatttttaattgatttcaactcttngtcnmttcagccattaa tgggatgactacagcttgcctggcctgaaat(g/a)tatgagcaagagtggtgggttacac ctgctgaacataagcgcctcccaagacattccagtggttcacttccagccagacacttgcctga aaatggcaataaagcaccagcttagggcttggccctcttgcctggttaagattgggttaattgg gaagggggccctgcctgaagaATACAGGAAAGGCAATCTG
F5u32	F5	T	G	F	V	cds	GE910	GCAGGTAATAT TGGTGTG	TTTACTGTATC AATGCCAGCT T	GCAGGTAATATTGGTGTGTCaat taatcagggaaacccacatgacaggtatgttccacacccctg ggatggaaatggaaagatagaagaaacagcaaatcagacttcttctg(t/g)taagaatctt ggtagggagattactgggaacccctccgctgcctgtaagctccagggcgtgtaactctt caagcgaagctcangtactctatctatgctggttctctctagggctccaaagaaacaaagggcc ctcactaccacaacatggaggtatctgggaagcagaggtattttaatctgtcttgcataa atcctaggtccaanagtcaggatgctggagactgatancttgaactataacttctgtctcaaa aanaagcttatactctctgttggcttcttctgatttgaatttaaccataataaagcaaat taatttcttgcaagggatanaatggtaaatctttagtcttggggccatacatctctgcca taactactCAACTGCTCATTTGTATCAGTAA
F5u33	F5	A	G	D	G	cds	GE921	AAAACCTTAG CCATTATGTT GT	AGAAAGAGAA ATAGTGAATA C	AAAACCTTAGCCATTATTTGTGTCatttaagattttctcttatttggcttccagatttttgaag gaataactaatcacaagagacatgtaagaacttttcaaccccccaactatttccaggtttatc cgtgctactctcaaaacatggaatcaaaatatttgcacttgcctggaaacttcttggctg(tg/a/g l)atttactgaattgaacattcaaaacccctggagagactctttaaagacctcaaacctatta gaatggggcaatgtattttagcgtgtttaaatttaacagTTTTCACATTTCTCTTTCTT
F5u34	F5	A	G	Q	Q	cds	GE932	TCTACTAGACT TCTGAAGATAT GAGAG	TGCCAANTTAC CCATAGAAAT	TCTACTAGACTCTGAAGATATGAGAGactctcttcttgaatgtgagaaatagatatggaat atgccccttcaaatgatttttcttatttctccagtttgaacttcttctgttaacttctttaaaga aaattgtctacagagatgtaaacatatttaagaagaagaaacacaca(a/g)lctacacttcc aggtaagcctgaaataactttttaaattttaaagataaTTTCTATGCTAATTTGGCA
F5u35	F5	G	A	A	A	cds	GE962	GCTATCCCGA TTTGAAGTGG T	TTTGTCCCATG ACAGAATCC	GCTATCCCGAATTTGAGAGTGGTgaacacgaactcctcagaaatgccacatgctcttgatggct gttactctccaggtgcttcttacttgaactgaacacatctccctg(c/g/a)gagaagatggacgacg ctggtgctccagggagaaatcacctatgaaatgagtagatcagtgaggacagtgggccacccat gatgacctccatgctccacacacatcttacttccatgaatgaatctgctgaggtattcaactc gggctgtagtgggcccctgcttctctgtaaaaaagggttaagaacaccccccccaaaagatccaaca actaaatgttggaaatgctcaGAGGTTCTGTCATGGGACAAA
F5u36	F5	G	A	V	M	cds	GE915	TGATTTATCAGA AGAGCAAGGAA A	ACTGTGACCCA GTGTGATTTA	TGATTTATCAGAAGCAAGGAAATtcttgagaagaaggaacataacttactgttttctccagg aaaagatatctactcaggtctgtagagctcccttcaacttgcctcaaaaggaata-tacataag gacagcaacatgctt(g/a)tggaagatgagaaatttcttactatttattgacctttgatgaa agaagagctggttactatgaagaagactcccaaggttcttggagactcacatctcagaaatgaa aaatccccatgagttccaggttatttctcctggactttgatctaactctctaatTAAATCACACTG GGTCCAGT

FIG. 5CCC

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
F5u37	F5	C	T	P	S	cds	GE391	CCCTTCTCAC CAACAAC	AGCACGTGAGG CATTCTGG	CCCTTCTCACCAACAGCACCACAGCTGGTCC[c/t]cactgagacacctcattggcagaagc558 ctcagttctcaattctccacgagagactccagcccatattctgaagccctatagagatc ctctacgacagatgtccagggatcgtctcttcttcttggctggagaaatcaggaatc gaacatgctaaagtgaaagcccaaggttagaagatcagagcaagacagacagctctctg gatgaattactagcacataaagttgggagacactaagcccaagacactggttctctctccgaa tgagccctgggagacctctctagccaagacactgggtctctctccagatgagccctggag gacctctagtgtactctctaaacaaagtaactcattcaagatttgggttgggagatg gcaattggctctggagaaggtagctatgaataatccaagatactgatgaagcacagctgtta gcaattggctgacagcccccCAGAACTCCCTACGTCT
F5u38	F5	G	C	E	D	cds	GE362	GCTATCCAG TTTGAAGTGG T	TTTGTCCCATG ACAGACTCC	GCTATCCAGATTGAGTGGTGAAGCAATCCTCAGAACTGCCACATgtctgatggct366 gttactctccagggtgtctctctcttgaccacatctctctggag[c/g]clagatggagacg ctgtggctccagcgagatacactctgaagatcagatgagatcagtgagagaccacacat gatgacctctcctcacacatactatctctcctgaaatctgatcgagattctcaactc ggggctgatgggcccctgtctatctgtlaaaaaggttaagacaacccccacacagattcaaca actaaagtgtggaatggctcAGGATCTGTCATGGACAAA
F5u39	F5	G	A	E	K	cds	GE391	CCCTTCTCAC CAACAAC	AGCACGTGAGG CATTCTGG	CCCTTCTCACCAACAGCACCACAGCTGGTCCCACTCAGACACTctatggcagaagactca gttctcaattctccacgagacatctcagccatactctgaagacctatcagagatcctct acagccagatgtcacaggatcagctctctcttctcttgggtggagaaatcagaatcagaac atgttaagcttaagggaaccccaaggtagaagagatacaagagacaaagcacaggtctctctggatg aaattactgcacataaagttgggagacactcaagcaagacactgggtctctctccggaaagg gccctgggagacctctctagccaagactgggtctctctccagatgagccctgg[c/a]ag gacctctagtgtcttctctcttaaaaagtaactcattcaagatttgggttgggagatg gcaattggctctggagaaggtagctatgaataatccaagatactgatgaagcacagctgtta acaaattggctgacagccccCAGAACTCCCTACGTCT
F5u4	F5	T	C	M	T	cds	GE172	TTTAAGAAAT ACAGGTCTCAG CAT	TTTCTCCCATG ATTCTGTATT GT	TTTAAGAAATACAGTCTCAGCAATTTggataattctcaacaaatctggaacactataaga aagttatgtcacacagtacagatgagtcctctcccaacatacagtgaaatcccaat[c/c] gaagaagaatgggaatttgggtctctatctacagagcccggtcagagacacactcaagtaagta ACAAATACAGAAATCACTGGGANA
F5u40	F5	C	G	P	A	cds	GE391	CCCTTCTCAC CAACAAC	AGCACGTGAGG CATTCTGG	CCCTTCTCACCAACAGCACCACAGCTGGTCCCACTCAGACACTctatggcagaagactca gttctcaattctccacgagagacatccagcccatctctgaagacctatcagagatcctct acagccagatgtcacaggatcagctctctcttcttgggtggagaaatcagaatcagaac atgttaagcttaaggga[c/g]ccaaggtagaagatacagatcaagcaagacaggtctctctg gatgaattactagcacataaagttgggagacactaagccaagacactgggtctctctccgaa tgagccctgggagacctctctagccaagacactgggtctctctccagatgagccctggag gacctctagtgtactctcttaaaaagtaactcattcaagatttgggttgggagatg gcaattggctctggagaaggtagctatgaataatccaagatactgatgaagcacagctgtta gcaattggctgacagccccCAGAACTCCCTACGTCT
F5u41	F5	C	G	L	V	cds	GE915	TGATTATCAGA AGCAACAGGAA A	ACTGTGACCA GTGTGATTTA	TGATTATCAGACAGAGAAATctctggagaagggcaatacaataatttactctgttttccagg aaaagatattctcactcaggtctgagaggtccctc[c/g]caactgcacaaagagata-taca taaggacagcaacatctgctatggacatggagaatttctctactattctatgactcttgatgaa aagagctgtgtactatgaagaagctccagagttcttggaactcacatctcagaaatga aaatccagaggttccaggtatttctctcggaacttgatctaatctctcaatTAATACACTG ccacacac

Poly Id	Gene	ref Nr	alt Nr	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer [5' -> 3']	Reverse Primer [5' -> 3']	Assay Sequence
F5u42	F5	T	G	Y	D	cds	GE279	GAATTTAGGCA GTGTGTGACTT G	ACAGATTTCAGA TAGAATAATGCG ACAC	GAATTTAGCGAGTGTGTGACTTGTCTGcagaaggacagctctgttttacttggtctttctataatgacg gtggacatgcaaaaggagatcaataacacagggatccagacaaagtcccaacacactactactgaa gtctgtctataccacaggttc[t/g]atgctctacagtttccacacagatcaactgtggcagac ttcaagggaacacgacaagaagtgtgatggtttgtgtgcacattatTTCTATCTGATCTCT
F5u44	F5	C	A	L	I	cds	GE395	GACCTCAGCCA GACAAACCT	TCTGATCAGG TCTGGAGGA	GACCTCAGCAGACAAACCTCTctccagaactcagtcagacaacacctttctccagcctcggtcga gatgcctttctccagactcagccatcaaacctttcttcagactcttcagactcagccacagcaaacctct ctccagactcagccatgatgactctctccagaactcagtcagacaacacctttccacagcctc ggtcagatggccatttctccagactcagccatcaaac[c/a]ttctctcagacttcagccagc caaacctctccagaactcagtcacaacacctttccacagcctcggtcagatgcccctttct ccagaccagccatcacacacctttcttcagactcagccagacaacacctctctccagaactcag tcagacaacaccttcccccagactcagtgagatggatggccctttctggcagactcagtcacaaattcccc ttacccagactccagcagatgacactttctccagactttggagacagatcttttcccaaac tttggtcagatgctcttccccagactcagccagtgactctctccagacatcagtgacac caccttctccggatctcgcagatataccctCTCTCCAGACTTGTATCAGA
F5u45	F5	T	A	L	I	cds	GE923	GATCATGCTTT TTCTTAGGTT	TTCCAGATTACG AGGTTAGGGGA	GATCATTTCTTTCTTAGGTTGgtttttaaataat[t/a]tagcatccagaccgtcttctctacatg ccatggactttctatgaaaatactcagagggaagaactctatgaagatgactctctcactgaatg tttaaggaaatataatgctgtctcagccaatagcagttatcactctatcagtcagccactgagcg atcagggccagaagctcgctctcgctgtcggtctgggcttgggctctactactcagctgtggaaccag taggtacttctaatgaaagtgtttctcaatTCCCTTACCCTTGTATCTGAA
F5u46	F5	C	A	L	I	cds	GE387	GTGCCCCACGA GGAACTA	TCATATGGCTG AGTTCTGGAG	GTGCCCCAGGAACTATcaaacatctcccatcagaacctctatcaagacctatcaaatgacttactctc agccccctcagatctctcttcagagctcagtgaaatgcttgaatgagccagatcactctc agctcttcccccacagatataaagtcataatctctctcagacatgaagttctggcagacagtc atctctccagctccagcaggatgacctctctcagaactcaggaactcagcagacaacacctctctccaga ctccagccagactctctccagaactcatcagaaaacctttcccccagcctctggtcaga tgccatttctccagactcagccatacaaccttttctccagactcagccatcaaacacctttct ttagactcagcagacaacacctctctccagaactcagtcagacaacacctttccagccctctgg tcagatgcccctttctccagactcagccatacaacct[c/a]ttctctcagacttcagccagaca aacctctCTCCGAACTCGACCTATGA
F5u5	F5	A	G	K	K	cds	GE172	TTTAGAAAT ACAGGTCTCAG CAT	TTTCTCCCATG ATTCTGTATTT GT	TTTAGAAATACAGGTCTCAGCATttggataattttctcaaaccaaatctggaaaaacattataaga aagttatgtacacacagtcagaagaatgagctttcccaacaacatcagtgaaatcccaatgaatga a/a]lgagaatgggattttgggtctctatactcagccagcctcagcagacaactcaaatgaatga acAAATACAGAAATCATGGGAAAT
F5u6	F5	G	A	E	E	cds	GE174	TCTATGGTCT GTTCTGTACC	CAACCACAGA ATGAAAMCTG	TCTATGGCTCTTCTTGTACCGactatactgtttgtctctccagaggcagcagacatcgaa cagcagggctgtgttctgtgtgttgacagacaacaaagctggactctggagacaacatcaacaa gttttggaaaactcctgatga]a]lgtaaacgtgatgaccacaagttttatgaatacaaacatc atgagcagaaagtcagatcactattttgttctcatCAGTTTTCATCTCTGTGTGTTG
F5u7	F5	C	A	T	T	cds	GE175	TTTACACTTT CAGTATCAAT GG	GCTTCTCTGT GAGTGTCCAG	TTTACACTTTACAGTATCAATGctatgtcgtctcagagacataactactcttttgatctgtctgtg atgacactctccagtggtcactctgtgagttgggacccagaaatgaattttgaccatctctgtg actgggcactctatctatgaaaggagcattgagacactctgac[c/a]tctctcccatgc gtggagaatctgtgcgggtccaatggataatgttgggtgagtaagagttCTGGAACTCATCAGNAGG

FIG. 5EE

[illegible]

FIG. 5FF

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
F7u3	F7	G	T	G	V	cds	GE412	CCCTGCAGACC TAGAATGG	CCGCATTAACT GCAGAGAATA	CCCTGCAGACCTAGAAATGGccacaccatccccatgcaccagggggtgaggtggcaggtgggtg gaaggggcctgaggggggctctctctccaggcgagcagcactcagcagcagcagcagcagggagtg agacagccgggtggcaggatcatctccacgacgctacgctccgggacacacacacacacac gacatgcctgctcgctgcaccagcctgctctactgacctatggctcagcggcttgccttgcct gcccagcagactctctgagagagcctggccttcgtgccttctatggctcagcggctggg gtcagctgtggacctggccacacccctggagctcgtctcaacgtgcccctggctgagt accaggactgctgcagcagctcaggaaggtag/lagactcccaaatcacagaglacac tgtctgtccggctactcggatggcagcaggactcctcgaaggggacagtgaggggccacat gccacctaccgggcacgtggtacctgacgggcatcagctgggggagggggctgcgaac cgtgggccactttgggggtatcacagggtctccagctacatcagatggctgcaaaagctatgc gtcagagccacccaggagctctctcgagcccatctccctagcccgagccctggcctg tgagagaaagccaaggtgctcgaaactgctctggaccacaaatcccatatATTTCTTCAGTT AATGGG
F7u4	F7	C	A	D	E	cds	GE412	CCCTGCAGACC TAGAATGG	CCGCATTAACT GCAGAGAATA	CCCTGCAGACCTAGAAATGGccacaccatccccatgcaccagggggtgaggcgaggtgggtg gaaggggcctgaggggggctctctccaggcgagcagcactcagcagcagcagcagcagggatg agcagccgggtggcaggatcatctccacgacgctacatcccgacgctgctccgggacacacacac gacatgcctgctcgctgcacacccgctgctctactgacctatggctcagcggcttgccttgcct gcccagcagactctctgagagagcctggccttcgtgccttctatggctcagcggctggg gtcagctgtggacctggccacacccctggagctcgtctcaacgtgcccctggctgagt accaggactgctgcagcagctcaggaaggtag/lagactcccaaatcacagaglacac tgtctgtccggctactcggatggcagcaggactcctcgaaggggacagtgaggggccacat gccacctaccgggcacgtggtacctgacgggcatcagctgggggagggggctgcgaac cgtgggccactttgggggtatcacagggtctccagctacatcagatggctgcaaaagctatgc gtcagagccacccaggagctctctcgagcccatctccctagcccgagccctggcctg tgagagaaagccaaggtgctcgaaactgctctggaccacaaatcccatatATTTCTTCAGTT AATGGG
F7u5	F7	C	T	T	T	cds	GE412	CCCTGCAGACC TAGAATGG	CCGCATTAACT GCAGAGAATA	CCCTGCAGACCTAGAAATGGccacaccatccccatgcaccagggggtgaggtggcagatggatg gaaggggcctgaggggggctctctctccaggcgagcagcactcagcagcagcagcagcagggatg agcagccgggtggcaggatcatctccacgacgctacatcccgacgctgctccgggac/laccaa ccagatcgcgtgctcgctgcaccagccgtggctctactgacctgacacatgggtgacctct gcctgccgaagcagcttctctgagagagcctggccttcgtgccttctatggctcagcggct tggggccagctgctgagacctggccacacccctggagctcgtctcaacgtgcccctggct gatgacccaggactgctgcagcagctcaggaaggtagggagactccccaaatcacagggatc tgtctgtccggctactcggatggcagcaggactcctcgaaggggacagtgaggggccacat gccacctaccgggcacgtggtacctgacgggcatcagctgggggagggggcagggctgcgaac cgtggggcactttgggggtatcacagggtctccagctacatcagatggctgcaaaagctatgc gtcagagccacccaggagctctctcgagcccatctccctagcccgagccctggcctg tgagagaaagccaaggtgctcgaaactgctctggaccacaaatcccatatATTTCTTCAGTT AATGGG

FIG. 5GG

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
F7u6	F7	A	T	E	V	cds	GE412	CCCTGCAGACC TAGAATGG	CCCCATTAACT GCAGAAGATA	CCCTGCAGACTAGAAATGGccacagccatccccatgcaccagggggtgaggtggcaggtgggtg gaaaggccctgagggggcctctctctccaggagcagcagcctcagcagcagcagcaggggagt agcagagccggcgggtggcggcagggtcatctcccacagcagctagctcccggggacacacacacac gacatcgctgctcgcctgcaccagccctgggtctctcaatgacacatggtggccccctctgctt ggcgaaaggacgttctctg(a/t)gaggacccctggcctctgctgctctctcaatgctcagcggc tggccagcagctgctgagcgtggcgcacggcctcctggtctctcaatgctcctcaatgctcagcggc gatgaccaggactgctgcagcagtcacggaagtgaggagctcccaaatatcacgagataca tgttctgtggcgctactcgatgcagcagcaggactctgcaaggggagctggaaggccacat ggccaccactaccggggacgtgggtacctgacgggcatctcagctggggggcagggctgcgcacac cgtggggcaactttgggggtgtacacagggtctcccagctacatcgagtggtgcgaaggctctatgc gctcagagcacgcggcaggagctctctctgcagagcccatctctctagccagagccctggcctg tggagagaaagccaaggctgcgtcgaaactgctctggcaccacaaatcccatatattttcttcacgatt AATGGGG
F7u7	F7	C	T	A	A	cds	GE412	CCCTGCAGACC TAGAATGG	CCCCATTAACT GCAGAAGATA	CCCTGCAGACTAGAAATGGccacagccatccccatgcaccagggggtgaggtggcaggtgggtg gaaaggccctgagggggcctctctctccaggagcagcagcctcagcagcagcagcaggggagt agcagagccggcgggtggcggcaggctcatctcccagcagctagctctccgggacacacacacac gacatcgctgctcgcctgcacagccgtgggtctctcaatgacacatggtggccccctctgctt ggcgaaaggacgttctctgagagagcgtggcctctgctgctgctctctcaatgctcagcggcgtggg ggcagctgtggaccgtggcgcacggcctggagctcatggtctctcaatgctcagcggcgtggg accagagctgctgcagcgtcacggaaggtgggagactcccccaaatatcacgagatgacatgtt ctgtgc/lc/l)ggctactcgatggcagaaggactcctcgaaggagcagctggaggccacat ggcaccactaccggggacactggtacctgacgggcatgctcagctggggggcaggcgtgcgcacac cgtggggcaactttgggggtgtacacagggtctcccagctacatcgatcgatggcgaaggctctg gctcagagcacgcggcaggagctctctctgcagagcccatctctctagccagcagcagcctggcctg tggagagaaagccaaggctgcgtcgaaactgctctggcaccacaaatcccatatattttcttcacgatt AATGGGG
F7u8	F7	T	A	V	D	cds	GE412	CCCTGCAGACC TAGAATGG	CCCCATTAACT GCAGAAGATA	CCCTGCAGACTAGAAATGGccacagccatccccatgcaccagggggtgaggtggcaggtgggtg gaaaggccctgagggggcctctctctccaggagcagcagcctcagcagcagcagcaggggagt agcagagccggcgggtggcggcaggctcatctcccagcagctagctt/ljccccggacacacacaa ccacagacatcgctgctcgcctgcacggccgtgggtctctcaatgacacatggtggccccctct gctcggcggcaggagcgttctctgagagagcgtggcctctgctgctgctctcaatggtcagcggc tggggcccgactgctggaccgtgggcgcacggcctggagctcatggctctctcaagctggccggct gatgaccagagactgctgcagcagtcacggaagggtggggagactcccccaaatatcacgaggtaca tgttctgtggcgctactcgatgcagcagagactcctcgaaggggagcagtgccggggccacat ggccaccactaccggggcagctgggtacctgacgggcatgctcagctggggcagagcgtgcgcacac cgtggggcaactttgggggtgtacacagggtctcccagctacatcgatcgatggcgaaggctctg gctcagagcacgcggcaggagctctctctgcagagcccatctctctagccagcagcagcctggcctg tggagagaaagccaaggctgcgtcgaaactgctctggcaccacaaatcccatatattttcttcacgatt AATGGGG

FIG. 5HHH

[illegible]

FIG. 5III

[illegible]

FIG. 5KKK

[illegible]

FIG. 5LLL

[illegible]

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
FGAu8	FGA	T	C	P	P	cds	GE414	GAGCCCTAACACCCAGACT ACCCAGACT	AAAAGGTGTAG TTTCAATGACG TGTA	821 GAGCCCTAACCCAGACTTGGGCGACATTGAGAGGCTGTCAGAGAAATGAAGTCAAGGACAA GGAGAGTACCACACAGAAAACGGTCACTCTGAAGAGATGAAGCTCAGGACTGGTAA GAAAGTCACCTCTGGTAGCACACACACCGCTGCTGATGCTCAAAACCGTACTAAGAG TGTATTGGTCTGATGGTCCAAAGATTTCCAAAGAGTGTGCAAGAGTGGTCACTCTGAAGAGT ACTGTCGGAGGAATGAAATTAGGCACTTCTGGTCACTGTTAGTCACTCTGATGGTCTCGCAT AGGCACCTC/GGATGAGCTGCTTCTGACACTGCTCACTGGAAAAACATCTCCAGGTT TCTTCACTATGTTAGAGAGTCTTCTGAGTGAAGTCTGAGTCTAGGGGCTCAAGATCTGGCAT TTCAAAATACAAAGGAATCCGTTCTCACTCCCTGGGATAGTGAATCTCTCCCTGGTAA ATCTCAAGTCTACAGAAACATTTACTAGTACAGCTTACAACAGAGAGAACACATTTG AAGCAAGAGCTAAAAATGGCAGATGAGGCGGAAGTGAAGCCGATCAAGAGGAACATAGC ACCAAGAGGCGCATGCTAAATCTCGCTGTCAAGGATCCCACTTCTCTCTGGGAGGCC TCTCTGCTCCCTAGCAAGTTAAATCTTCTGACAGTGTCCCATGCGCCTTGTGCTTCTC TTCTAACTCTCTGTTACACGCTCAATGAAATACACTTTT
FGAu9	FGA	G	C	S	T	cds	GE415	TTAACTACACG GAACTCAATAG ACG	CTGACACCTCT TCAATGTGCG	825 TTAACTACACGAACTCAATGACGAGTATTGATTTGATCTACATCTTCTCTTCTTCTC TCCCTCTCTAGGTGGACATGATATAAGATACGATCTGTGGAGGTCTGACGTAGGCT TTAGCTGTGAAGTAGCTGAAGACTATGAAGTCAAGTACAGAGAACGACTGAACAGTCACTGC CAAGACTTACTTCCCTAGATAGCAACACTTACCCTGATAAAAATGAACCAAGTCTCCAG ACTTGTCTCCGAAATTTTAAAGCAGCTCAGAAGGTACCCCTGGGAGGAGGCATTAA GACATCGCAGATGAGAAATGGGTAGGAGACTGGTGGAAATGAGTTACTGCGAGGCTC CACTCTTAGGAACGGATCAGAGCGAAAGCCCGAGAACCTCTGACGTCTGGAAGCTGGA ACTCTGGAGCTCTGGACCTGGAAGTACTGAAACCGAAACCTCTGGAGCTCTGGAGCTG ACTGCAACTGAAACCTGGAGCTCTGGACCTGGAAGTACTGGAAAG/CTCTGGAACTCTGGGA GCTCTGGAATGGAGTACTGGAACCAAAACCTCTGGAGCCCTAGACCTCTGGAGCTCTGATCTGG TGGAACTCTGGAGCTCTGGAACGGAGCTCTGGAGCTCTGAGCTCTGAGAGCTCTGATCTGG TAGACTGGCAATGGCACTGATCTGGAACTTTTAGGCCAGATAGCCAGGCTCTGGGAACG CGAGGCTCAACACCCAGACTCTGGCACATTTGGAAGAGGCTCTG
FGD12	FCB	T	A	-	-	noncoding	GE336	GTAACCATTC TGAAGTCATTC CT	CAATTCATTT CATAACTATA GCAA	314 GTAACATTTCTGAAGTCATTCCTAGCAGAGACT/a/cagatatataagattgaagatctctc tcaagttaagctctacatgaaaagatggcttcttgagactctcccaacttaaaacatgaacaa tctattatgtctactatgtgtgttttcttagttaagtcctcaaggtgtcaacgacaatgagggg tgaatttttaagcattattattatcatgtagtattattataataagatgtaacataatcata ttagtgcctattttaaagaattagcatTCGTTATAGTTATAGTATGAAATCGAATTC
FGD13	FCB	A	G	K	E	cds	GE336	GTAACCATTC TGAAGTCATTC CT	CAATTCATTT CATAACTATA GCAA	314 GTAACATTTCTGAAGTCATTCCTAGCAGAGACTCAGATATATATAGGATGAGATCTCTCAA gttaagctcacatg/a/gaaagagtggtttcttggagctctcccaacttaaaacatgaacaa tctattatgtctactatgtgtgttttcttagttaagtcctcaaggtgtcaacgacaatgagggg tgaatttttaagcattattattatcatgtagtattattataataagatgtaacataatcata ttagtgcctattttaaagaattagcatTCGTTATAGTTATAGTATGAAATCGAATTC
FGD14	FCB	T	A	-	-	noncoding	GE336	GTAACCATTC TGAAGTCATTC CT	CAATTCATTT CATAACTATA GCAA	314 GTAACATTTCTGAAGTCATTCCTAGCAGAGACTCAGATATATAGGATGAGATCTCTCAA gttaagctcacatgaaaagatgggtttcttgagctctcccaacttaaaacatgaacaa tctattatgtctactatgtgtgttttcttagttaagtcctcaaggtgtcaacgacaatgagggg tgaatttttaagcattattattatcatgtagtattattataataagatgtaacataatcata ttagtgcctattttaaagaattagcatTCGTTATAGTTATAGTATGAAATCGAATTC

FIG. 5NNN

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
FGBd15	FGB	C	T	P	L	cds	GE350	TTTCAAGGTC TATAATACAC ACTCC	ACACCTGGCCT TGTTTCTCG	TTTCAAGGCTCTATATATACACACTCCTtagtaacctatgtaattgtttattttaagaatttggtga ctaaatacaagtaattatgtcataaaccttgaaataatgtgtttcttacctttgcagaattgtg aggaattatcaggaagaaggtggaacatctgtaaatgtatctctcattcaactgcagctctgttc aaac[c/l]gtatagagatcgtgacatgaatacagaaaatggaaatgaagcttccagacagttg ttgacctgttgatctgtaatttttgggtacacgtataaagtcCAGGAACCAAGGCCACAGTGT
FGBd16	FGB	T	C	C	C	cds	GE351	GGCTGAATTTT CCTATGTGCTA TT	TGCAATTCCT GGCAGTCTA	CGCTGAATTTTCTATGTGCTATTTtaacaaatgcccataagcccaactctcatcctaagctcg ctattcttctgttttaggggtgtgtg[c/l]cctcacaggatgcagttgcagaaggtctgtgtac ctacaacaggaaagcccaatcagaatagtg[c/l]gtatagagatgcagttgcagaagctgtttg ccagactctctctcttccttcagtaactgtttgtgaaagccctggtgcacaaagggcaga agcaagtaaaaggtagatatcctgtgtcttcattcgatttcagctataaataatggaaacctT AGACTGCCACGAGATGCA
FGBd17	FGB	T	A	-	-	noncoding	GE392	AAGGGAAGAA GGCAGTTTT	CCCAGGAAGTG GTAGCTATTAA A	AAGGGAAGAAAGGCAGTTTTtagtttcccaaaattttatttttggtagagattttattt[c/l] gtttcttcttagtgtaattgtctggaataataaatttagccagctaccagagctgggacc cacagaactttgatagaaatggagactggaagagacaaaatgaagctcaactatggagagat tcactgtacagaatgaagcccaaataccagatctcagtgaaacaatacagagacagccggg aatgcccctaggttaggcactctcagctgtatgggaagaaacagagacatccacaacgg catgtcttcagcargatgacagagacaatgacgctgtgtatgtgtgacactcttctcctgc tttaaaatcacactaatatcattactcagaatcatttaacaatatTTTAAATAGCTTACCACTTCC TGGG
FGBu1	FGB	C	T	S	S	cds	GE390	TCATAACTGCT TGGTGATAGCT C	CCACTTAGCAT TTTTGTGTGTG	TCATAACTGCTTGCTGATAGCTCagtggttaatagtttattctcagaaaaatacaaatgtgatagt taaatcacattagttttatgagccaaaatgctaaactattctcacaataattctattttccagata atgaaaatgtagtcaaatgagtagtactctcagaactggaaaagcccaattatataatagtgagact gtgaatag[c/l]taatatcccaactaaccttcgctgtctgttcttaacttcggaacacctgaaa gcaaatcaaaaagtttagaatctgatctcagctcaaatggaatttcgcaaccccatgcaat gtcagttgcaatatcctgtgtgtctggcaaaagttactcgtattcaacaatatcttttagagag ttccagaagaactcacacacaaaataagagaacaacaaCMACMAAAATGCTTAACGG
FGBu10	FGB	G	T	S	I	cds	GE351	CGCTGAATTTT CCTATGTGCTA TT	TGCAATTCCT GGCAGTCTA	CGCTGAATTTTCTATGTGCTATTTtaacaaatgcccataagcccaactctcatcctaagctcg ctattcttctgttttaggggtgtgtgtcctcacaggatgcagttgcagaaggtctgtgtac aaacaggaaagcccaatcagaataa[g/l]gtgtatgagttaaaatacaagctgggaagctgtttc ccagactctctctcttccttcagtaactgtattgtctgaaagacatggtgcacaaagggcaga agcaagtaaaaggtagatatcctgtgtcttcattcgatttcagctataaataatggaaacctT AGACTGCCACGAGATGCA
FGBu11	FGB	A	G	S	S	cds	GE392	AAGGGAAGAA GGCAGTTTT	CCCAGGAAGTG GTAGCTATTAA A	AAGGGAAGAAAGGCAGTTTTtagtttcccaaaattttatttttggtagagattttattttgttc ttcttttagtgtaaatgtgcttggaatgataaaatttagccagctaccagagtgggaccaca gaactttgatagaatggagactggaagagacaaagttaaagctcaactatggagagattcac tgtacagaatgaagcccaaataccagatct[c/l]gtgcaacaatacagaggaacagccggc aatgcccctatggtaggcactctcagctgtatgggaagaaacagagacatccatttcacaacgg catgtcttcagcargatgacagagacaatgacgctgtgtatgtgtgacactcttctcctgc tttaaaaatcacactaatatcattactcagaatcatttaacaatatTTTAAATAGCTTACCACTTCC TGGG

FIG. 5000

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
FCBu2	FCB	A	T	E	V	cds	GE390	TCATACACTCTTGGTGATAGCTC C	CCACTTAGCAT TTTTTGTGTG	TCATACACTCTTGGTGATAGCTCAGTGTCTTAATAGTTCTCTTCGAGAAATCAAAATGTGATAGTAAATCATTGTTATGAGGCAAAATGCTAACTATTTCTTCATATTTCTCCAGATATG/a/TTAAATGTAGTCACTCTCAGAACTGGAAGCCCAATATATAGATGACTGGAATAGCAATCCCAATCACTCTCGTGTGTTCACTCTCGGAAACCTGGAAAGCAATACAAAGTGAATCTGCTCAGTCAATATGGAATATTTGCAACATATTTAGAGTTCCAGAGAACTCACCAAAATGAAGAGCAACAACAACAACAATAATGCTTAACTGCG
FCBu3	FCB	G	T	V	V	cds	GE330	GGGATTCAGAT ATTATTTCAA ACTG	GCTTCCACAA TGAATGTTTT	GGGATTCAGATATTATTTCAAAGTCACTATTTGCTGTGGTAAATATATCTCTCTTTGTTCTGCTCAACCAAGGATGGACAGTIG/ATATCAACCTGCTCAAGAGCTGACTTGTACTTTGGCAATGGGATCCATATAACAGGATTTGGAATGTTGCAACCAACAGATGGGAAGATACGTGGCTACCAGGTAACGAACAGCATGCAAAATAAATCATCTCTATTTGAAATGGGATTTTTCTAAATAAACAATTCATTTGTAAGG
FCBu4	FCB	G	A	R	K	cds	GE382	ATGGGTAACT GCAAAAGTA	TCAAAAGTCA CACTACGCTCT G	ATGGGTAACTGCAAAAGTAACTTGACCACCTGATCTGTCTTCTTAATAAAGCCCAACACATTTCTCTCAGGTAACTCAGATCCCAAGAACCTGTCTTAAGAAGAGGTTGGTGGTGGTAAATAGATGTCAGCACTCAACAGCGAGACTACTAGTGGGTGGACAGTACACTCTGGGACATGGCAAGCATGGCAAGATGGTGTAGTATGAATGAATGGGAAGGCTGATGCTACTCAATG/a/ATGAAGATGAGATGAGATCAGGCCCTCTCTCCACAGCAATAGTCCCCAATACTGATATTTGCTCTCTGTGTGCAACATTTGTAGATTAATGTTATGGAAATTTCTCTCATACTATATCTCTAAACTCTCAAGCAGAGTGAAGTGAATTTTTGA
FCBu5	FCB	T	A	G	G	cds	GE477	GAATAGTTACA TTTCAAACTCT CTA	TGACTACAGC TTTTCTTCGAT	GAATAGTTACATTCCAAACTCTCTTAACACTCTGTATATATCTCTGCTCATCTCTCTGTAGGGTCTCTCTCAGTGCCTGGT/a/ATCATCGACCTCTGCAAGAGAGAGAGGCTCCCAAGCTGAGGCTGCCCACTCAGTGGAGTGGCTATCGGCTCGTCCAGCAAGAGCTGCCACTCAAAAGAAATGAAAGAAAGCCCTGATGCTGGAGCTGTCTCACTGACCAAGCACTGGTGGGTGACTGTATCTCTGCTGAGTGGCTCTCTCTGACAGAAAGCTCTGTATGCTCA
FCBu6	FCB	A	T	A	A	cds	GE330	GGGATTCAGAT ATTATTTCAA ACTG	GCTTCCACAA TGAATGTTTT	GGGATTCAGATATTATTTCAAAGTCACTATTTGCTGTGGTAAATATGCTCTCTTTGTTCTCTCAACCAAGAGATGGACAGTGAATCAGACCTGCAAGAGTATGTTGACTTTGGCAGAAATGGATCATAAACAAGGATTTGGAATGTGTC/a/TTCAACCAAGATGGGAAGATTAATGGGCTACCAGGTAACGAACAGCTGCAAAATAAATCATCTCTATTTGAAATGGGATTTTTCTAAATAAACAATTCATTTGTAAGG
FCBu7	FCB	A	G	R	R	cds	GE477	GAATAGTTACA TTTCAAACTCT CTA	TGACTACAGC TTTTCTTCGAT	GAATAGTTACATTCCAAACTCTCTTAACACTCTGTATATATCTCTGCTCATCTCTCTGTAGGGTCTCTCTCAGTGCCTGTG/a/ATGCTCTGCAAGAGAGAGAGGCTCCCAAGCTGAGGCTGCCCACTCAGTGGAGTGGCTATCGGCTCGTCCAGCAAGCACTGCCACTCAAAAGAAATGAAAGAAAGCCCTGATGCTGGAGCTGTCTCACTGACCAAGCACTGGTGGGTGACTGTATCTCTGCTGAGTGGCTCTCTCTCAGAGAAAGCTCTGTATGCTCA
FCBu8	FCB	C	T	II	II	cds	GE477	GAATAGTTACA TTTCAAACTCT CTA	TGACTACAGC TTTTCTTCGAT	GAATAGTTACATTCCAAACTCTCTTAACACTCTGTATATATCTCTGCTCATCTCTCTGTAGGGTCTCTCTCAGTGCCTGTGACTGCAAGAGAGAGGCTCCCAAGCTGAGGCTGCCCACTCAGTGGAGTGGCTATCGGCTCGTCCAGCAAGCACTGCCACTCAAAAGAAATGAAAGAAAGCCCTGATGCTGGAGCTGTCTCA/CTGCTGACCAAGCACTGGTGGGTGACTGTATCTCTGCTGAGTGGCTCTCTCTCAGAGAAAGCTCTGTATGCTCA

FIG. 5PPP

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Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
FGBu9	FCB	C	T	Y	Y	cds	GE392	AACGGAAGAA GGCAGTTTT	CCAGGAAGTG CTAGCTATTAA A	AAGGGAAGAAGCAGCTTTTtagtttcccaaatcttatttttggtagagattttatttttggttt tcttttaggtggaatttggcttgggaatgataaaatagccagcttaccagatgggaccacaca gaacttttgatagaaatggagagcggaaagggagcaaaagcctcaactatggagattccac tgtacagatgaagccacaaatccagatctcagtgagcaaaatc/tlagaggaaacccggt aatgctctcatggatggagcattctcagctgtaggagaaacacagaccatgcacacgg catgttcttcagcacgtatgacagagacaatgacggctggtatgtgtggtcacttttgcctctgc tttaaaatcacactaatatattctcaggaatcatcaaaatatttTTTAATAGCTTACCACTTCC TGG
FGd3	FGG	A	G	M	V	cds	GE337	TTCTGAATAGA CAGCTCTTCAT AGACT	GCAGTTAATTT TCTACAAATCA TCC	TTCTGAATAGACAGCTCTTCATAGACTTgcagaggtaaaagattccagaataatgatgtaca tctacgacttggttttaggtggcacttactcaaaagccttactcctcaatggctatgataatggca ttatttggccacttggaaaccccggtgtgtatctcatgaagaaacccact(a/g)tgagataat cccaatcaacagactcacaaatggagagagacacacacccctggggggagccaaacaggtcca gaccagagcaccctcggaacacagaatattgactcactttaccctgagagatgattTCTAGCAAAATT AACTGC
FGd4	FGG	A	G	-	-	noncoding	GE349	AAATACTTAG CAGTTTCCAAA GAAAA	TGGTAGCCAC TTCTTAAACTA TTC	AAATACTTAGCAGTTTCCAAAGAAATattctctggaaatgaatgttactacatgllanaagcta cttcttattttgttctatcttcttctgtttgtagatttttcaggaaatataataatcaaat atcaaaagattgttaacctgaagagagagtagccagcttgaagcacagtcgccagaaaccttgc aaacacacggtgcacaaatccatgatatacctgggaaaggaactgactgtagaggttatattgggatta ggttcatcaaaagttaagttaattgtaaggagaaagtattgactgg(a/g)aagtatagCAATAGTTTT AGAAAGTGGCTTACCCA
FGd5	FGG	G	A	G	R	cds	GE360	TGCTGATGTGA AAAGTAAGAAA AT	CAAGGTGCTTA GAAAAGTATCT GC	TGCTGATGTGAAAGTAAGAAATattctctggaaatgaatgttactacatgllanaagcta tttttcaaggtgggcacagcttcttaccctgatttcaaacacagcaaaagtgcgattctctctct agattgtcaagacattgccaaataaagagagctaaacagagc(g/a)ggcttcttcttcttctctct ctgaagctaaacagcaattcttactgtgaaatcgatggctggatggatggatggatggatggat gttccagaggttaatttttcccccacatgltatttaataaattctctacatgttctctgccata TGGCAGTACTTTTCTTACGACCTTG
FGd6	FGG	T	A	-	-	noncoding	GE372	GAACCACTGCT CTGTATTTTGG AC	CCATTGTCTAT TGATAGTTGGA AAG	GAACCACTGCTCTGTATTTTGGACaaattgttgcagcatctctcttaca(lt/a)gcattgatag tctatttctctcttcttct aaaaactggattcaaatataaagagagatttggacatctgtctctctctctctctctctctctctct gctgggaaatgagaagattctatttgaagaagcacacagctctgcccacatcccatatcatttaagagtg aactggaaagactggaatggcagaaccaggtactgttttgaatgacttccaacttttatttggtaa ggattgctgggaatgtgactTTTCCAACTATCAATAGCAANTGG
FGu1	FGG	A	T	Y	F	cds	GE404	CATCTACGAA AGAGGAACTT	TCCACTTCCAG TTTCAAGAAC T	CATCTACGAAAGAGGAACTTctgagatccctggaggggtcagcatgtgattgttatttcc tcttctcagactgcagact(a/t)tgccatgttcaaggtggagctgagctgagctgagctgagctgag ctcaacatagctactctgctgtgtgggtgctggtgagcttcttgaatggcttggatttggcg atgatcctagtgaacagtttttccatcccatatccatgcatgcatgcatgcatgcatgcatgcatgcat aatgataagtttgaaggaactgtctgaacaggtgagctgtgttggtaggaacaagtgctca cgctggccatctcaatggaggttattaccaaggtatgttttcccttcttcttcttcttcttcttcttct tatagtgatactatttccataaaataatataatatttccactaAGTCTTCTTCAACTTGAAGTGA agatagtagggattttatcatgttcttatttccactaAGTCTTCTTCAACTTGAAGTGA

FIG. 5QQQ

SUBSTITUTE SHEET (RULE 26)

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[illegible]

FIG. 5SSS

[illegible]

FIG. 5TTT

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
GABRB1 1	GABRB1	C	T	A	A	cds	GE1134	CTCTCAATCT TGAAAAAGA	GAGAGCCGAG GCATCAT	CTCTCAATCTTGAAAAAGAAccttaataagtgaggcaaccttcagctcaagcttcaggtatgtgtcttctctctca caggataccagcgggtgtcttaacatgacaacacatcagcaacccactcaggagagacccctgcgcaag atccctatgtcaaacggcgtatgtatctatgtatgggttgcttgggtgtgtgtcttctctctctctct gctggagatg(c/t)tttgtaattacatctctcttctggaaaggccctcagaaaaaggagct agcaacagcagcagtgccaatgagaagataaactggagatgaataaayccaggcaagata ttaaattctcaacatcttcttgaatttctcagcatCATGATTCCTCGGGCTCTC
GAP43d 3	GAP43	G	A	V	I	cds	GE1166	TCATTGAAGCC CTCTCTTT	TTCCCATCCA CCCATTT	TCATTGAAGCCCTCTCTTTttttctcgaagaaggttgaaaaaattgagacacacaaagattg aacaagatggatcaaacagagaataagctcaagcgcgaacacaaattcaggtagcttc cgtgacacataaacaggaataagctcaagagagaagaagatg(a/t)tcgaagctgtg aggctgaagctataaagaagatgaagccctgttgcgattgggttggaagaagaaggc acctactgcgaagcagcccgccctggctccaagctgatgagcccggaagcagaga aactctctcggagagaaggggggggtgctgcccacagagcagcccccaggctc ctgcatctcagaggagaagccgctcagctgagacagaaagtgcctcaacttccactgat aactcggctctccaagctgaagatccccagcgaaggagagcttaaaacagccgatgtgcc tgctgctgaactgctgctgcccacacccctgcccgagagatgctgtgcccaaggcaacag ccagcctccaacggagactggggagagcgaagcgaagctgaagagaacataggtagcaccgcga gggtcagatgcaATGGGTGGATGGGAA
GAP43u 1	GAP43	T	A	R	R	cds	GE1166	TCATTGAAGCC CTCTCTTT	TTCCCATCCA CCCATTT	TCATTGAAGCCCTCTCTTTttttctcgaagaaggttgaaaaaattgagacacaaagattg aacaagatggatcaaacagagaataagctcaagcgcgaacacaaattcaggtagcttc cgt(a/t)ggacacataaacaggaataagctcaagagagaagaagatgctccaagctgtg aggctgaagctataaagaagatgaagccctgttgcgattgggttggaagaagaaggc acctactgcgaagcagcccgccctggctccaagctgatgagcccggaagcagaga aactctctcggagagaagaaggggggtgctgcccacagagcagcccccaggctc ctgcatctcagaggagaagccgctcagctgagacagaaagtgcctcaacttccactgat aactcggctctccaagctgaagatccccagcgaaggagagcttaaaacagccgatgtgcc tgctgctgaactgctgctgcccacacccctgcccgagagatgctgtgcccaaggcaacag ccagcctccaacggagactggggagagcgaagcgaagctgaagagaacataggtagcaccgcga gggtcagatgcaATGGGTGGATGGGAA
GAP43u 2	GAP43	G	A	E	E	cds	GE1166	TCATTGAAGCC CTCTCTTT	TTCCCATCCA CCCATTT	TCATTGAAGCCCTCTCTTTttttctcgaagaaggttgaaaaaattgagacacaaagattg aacaagatggatcaaacagagaataagctcaagcgcgaacacaaattcaggtagcttc cgtggacacataaacaggaataagctcaagagagaagaagatgctccaagctgtgagggc tgaagctataaagaaggaagaagccctgttgcgattgggttggaagaagaaggcaca ctactgcgaagcagcccgccctggctccaagctgatgagcccggaagcagagagaact ccttcgagagaagaaggggggtgctgctgcccagagcagcagcccccaggctcctgc atcctcagaggagaagccggctcagctgagacagaagtgccactaaagcttccactgaact cgccgtctcccaaggtgaagatgcccagcgaaggagga(g/a)ctcaaacagccgatgtgcc tgctgctgaactgctgctgcccacacccctgcccgagagatgctgtgctccaaggcaacag ccagcctccaacggagactggggagagcgaagcgaagctgaagagaacataggtagcaccgcga gggtcagatgcaATGGGTGGATGGGAA
GHI1d7	GHI1	G	T	-	-	noncoding	GE509	GGGGGAGACT GTAGTCAG	GTCAATGGGC TCCAAATT	GGGGGAGACTGTAGTCAGccccggggcagcagcccaatgcccttcttccctgcgaac ctagagctgctccgaatctctctgtctctcaatccagtcgtggctggagcccgctgcaggttctccag gagtgctctcccaacagcctgtgtacggctcctgacagcagctcatgagcctctcaag acctagaggaaggaatcccaacgctga(ggggggtgggggtggcgttaggg(g/t)tcgcccaATCT TGCAGGCCCATTCAC

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
GHI1		G	A	-	-	noncoding	GE527	AAGGGCCAGG GTATATAAA	TCTCCCTCAG GACACATTG	AAGGGCCAGGGTATAAAAGggcccaagagacg [g/a] gctcaagatcccaagggcccaact ccccaaacctcagggtctctgagacagctcaactagctgaatgggtacaggttaagcgccctt aaaaacccttctggggcCAATGTGTCCTGAGGGGAGA
GHI2		A	C	-	-	noncoding	GE527	AAGGGCCAGG GTATATAAA	TCTCCCTCAG GACACATTG	AAGGGCCAGGGTATAAAAGggcccaagagacgggctcaaggatccccaggcccaactcccc g[a/c] lacactcagggtctctgagacagctcaactagctgaatgggtacaggttaagcgccctt aaaaacccttctggggcCAATGTGTCCTGAGGGGAGA
GHI3		T	G	-	-	noncoding	GE527	AAGGGCCAGG GTATATAAA	TCTCCCTCAG GACACATTG	AAGGGCCAGGGTATAAAAGggcccaagagacgggctcaaggatccccaggcccaactcccc gaacactcaagggtctctgagacagctcaactagctgaatgggtacaggttaagcgccctt aaaaacccttctggggcCAATGTGTCCTGAGGGGAGA
GHI4		C	G	S	C	cds	GE609	GGGGAGACCT GTAGTCAG	GTCAAGTGCGG TCACAGATT	GGGGAGACCTGTAGTCAGAGccccgggcagcagacggcccaatggccgtctctccccgcagaac ctatagctgctccgactct [c/g] cctggctctcagctcagctggctggagcgcccgtagcttcc caggaggtcttcggccacagctgggtgacggcctctgacagcaactcctatgacactccta aagggactgagggaaaggatcccaacgtgtaggggtgggggtggcgtgaggggtccccAATCT TGAAGCCCACTAC
GHI5		A	T	-	-	noncoding	GE527	AAGGGCCAGG GTATATAAA	TCTCCCTCAG GACACATTG	AAGGGCCAGGGTATAAAAGggcccaagagacgggctc [a/t] aggtcccaagggcccaact cccgaacactcagggtctctgagacagctcaactagctgaatgggtacaggttaagcgccctt aaaaacccttctggggcCAATGTGTCCTGAGGGGAGA
GHI6		G	C	-	-	noncoding	GE527	AAGGGCCAGG GTATATAAA	TCTCCCTCAG GACACATTG	AAGGGCCAGGGTATAAAAGggcccaagagacgggctcag [g/c] atcccaagggcccaact aaaaacccttctggggcCAATGTGTCCTGAGGGGAGA
GHI9		C	G	-	-	noncoding	GE602	GCTACACATG ATTTTGGAC A	GCTTCCCACT TATTAGTCT	GCTACACATGATTTTGGACtaatactcttttttaacctctctcttggagaacactcaagaa tggactcaagaatggaaagaatggcctgattgttctctggggaaacagctgttactttaa ttcatggttacctctctgataacttallgtatacgaactacgaatgggtgacagtggtatgag atgaaagtgttctctctgtatgaaatagglaaaatcacaggttttctgttctcaattgacatagtt t [c/g] AGACTAAATAAATGGGAAGC
GHI7		G	A	R	H	cds	GE597	TTGAGTTGTTG ACTCTTTGGC	TGACAAAGCC AGGTTAGC	TTGAGTTGACTCTTTGGCcaatctggcctttatatttttcttggaaagtgagccctatct tggacactcagttccagctgactcattgaaagtggataaaggaatatgaatgc [g/a] tggtag atccaaacaaagaaacttgaaaatatggcgaggttcagtgaggtgctctatgtaacacttctc agatgagccaatttacctggaagaaggttaaaagaataaaagatctaaatagtagGCTAACCTGG CTTTGTGCA
GHI8		C	T	-	-	noncoding	GE597	TTGAGTTGTTG ACTCTTTGGC	TGACAAAGCC AGGTTAGC	TTGAGTTGACTCTTTGGC [c/t] aatagggccttataatttttggcttggaaagatgagacctt atatatgacaacactcagttccagctgactcattgaaagtggaatgaagaatgagtggtggtag atccaaacaaagaaactctgaaatattggatgtcagtgaggtgctctctatgacacttcttc agatgagccaatttacctggaagaaggttaaaagaataaaagatctaaatagtagGCTAACCTGG CTTTGTGCA
GHI1		A	G	G	G	cds	GE596	TTAAATTTGCT CTGTCGTGTA CT	GAAGAAGAGT CAAAGTGTAAAG G	TTAAATTTGCTCTGTCGTACTaaatgctctgttgaaatgcacagtcgacacagatcccccat tggcctcaactcagcttactgaaactcagtttaactgaggtatctgacatctccagatctccagtgagat gggaagcaccacagatcagatattcagaagg [a/g] tggatgattcttgagatctgaacttca atacaaagaagtaaatgaaactaaatggaaatggtaagatgttgctacaCCTTTACACTTTGACT TTTTCTT

FIG. 5VV

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
GHRU2	GHR	A	C	I	L	cds	GE649	GCCCATATTCA GCTAAGCAAT	ATTGCCCCAGT CAATTTCTTT	GCCCATATTTCAGCTAAGCAATCCcaagttccactgctcaaacatcgactttttatgccacaggtgagcga cattacaccagaggttagtgggtctcttccccggggccaaaagaataaggcaggagatgtcccaat gtgacatgccccgaaatggtctctactctcccaaaaacttcttatggacaaatggactctctc tgtgagcagatgccaaaagtg/c ctctctgtgctctctctacatccttaccactgctggg tacgcccaagcttaaaccaagagacatttaccaccacagaaagccttaccactgctggg aggctgggacaggaagacattgtctccaggttctcagatgctgctccagactactccatctc tatagtcagctccccacaggccctacactaatgcagctgcttgccttggctgacaaagagt ttctctcatgtgctatgtgacagaccacacaaatcatgcttgagcttctctt ggttcccaagagctacgtatttaagagCAAGAAATTGACTGGGCCAAT
GHRU3	GHR	G	A	R	II	cds	GE596	TTAATAATTGTGT CTGTCTGTGTA CT	GAAGAAGAGT CAAAAGTGAAG G	TAAATAATTGTGTCTGTGTAATaagctctgttgatgacagctgcaaccagatcacccat tgccctcaactggactttactgaagctcagtttaactggatctatcgatctacaaagtagat gggaagaccac/g a caatgcagatattccagaagatggatggtctctggagatgacttca atcaagaagagtaaatgaaactaaatggaaaatggtgaagtgtgtctacacCTTTACACTTTTGACT TTTCTTTT
GHRU4	GHR	G	T	C	F	cds	GE1207	GCCATTTCATCA TAGCTATAAAC C	CTCACCTGGC ATMAAGT	GCATTCATGATAGCTATATAACCCgaattccacagtgatgactcttgggttgaaatttattgagct agatatgtagccagatgaaagactgaggaatcacagacagacagactctcccaagcagtgacc atgagaatacacatgactaactagggtggaagatggcgactctggagctaccagctgttgtaa ctgacattctgagagctgatttcaatgccaaatgacatcatatgagggttaccctggaggtgtcca gccacagaggttaaaagggaagcagatctcttatgcttgaccagaagaatcaataaactcac cttatcatgctt/g t ccctgctactcagcagccaggtgttatccagcagagagaacaa accacaaccacttctactgaagagctgagtcacactcacaagctgccccatcttcagctaaagca atcccaagttcactgtcacaacatcgACTTTTATGCCAGGTGAG
GHRU5	GHR	C	A	P	T	cds	GE649	GCCCATATTCA GCTAAGCAAT	ATTGCCCCAGT CAATTTCTTT	GCCCATATTTCAGCTAAGCAATCCcaagttccactgctcaaacatcgacttttatgccacaggtgagcga cattaca/c a cagcaggtagtggtctcttccccggggccaaaagaataaggcaggagatgtccc caatgtgacatgcccccgaatggtctctactctggccgaagaacttcttatggacaaatggacta ctctgtgagcagatgccaaaagtgctacctgtgctctccatcctcactcaggtgtgaatcacaca tacaccaagcttaaaccaagagacatttaccaccacagaaagccttaccactgctgctggg aggctgggacaggaagacattgtctccaggttctcagatgctgctccagactactccatctca tatagtcagctccccacaggccctacactcaatgcagctgcttgccttggctgacaaagagt ttctctcatgtggtctatgtgacagaccacaaatcgacaaatctagctttagcttctctt ggttcccaagagctacgtatttaagagCAAGAAATTGACTGGGCCAAT
GHRU6	GHR	C	A	P	T	cds	GE649	GCCCATATTCA GCTAAGCAAT	ATTGCCCCAGT CAATTTCTTT	GCCCATATTTCAGCTAAGCAATCCcaagttccactgctcaaacatcgacttttatgccacaggtgagcga cattacacacaggttagtgggtctcttccccggggccaaaagaataaggcaggagatgtccccat gtgacatgcccccgaatggtctcactctggccgaagaacttctcttatggacaaatggactctc tgtgagcagatgccaaaagtgactctgtgctctctcactcactcaggttgatctcacatcaca gcccaagcttaaaccaagaggaacttaccaccacagaaagccttaccactgctgctgggagg c/a ctgggacaggaagacattgtctccaggttctcagatgctgctccagactactactctcactca tatagtcagctccccacaggccctacactcaatgcagctgcttgccttggctgacaaagagt ttctctcatgtgctatgtgacagaccacaaatcgacaaatctagctttagcttctctt ggttcccaagagctacgtatttaagagCAAGAAATTGACTGGGCCAAT
GHRU7	GHR	G	C	W	S	cds	GE599	TCAACTTCTGTC TGATCTAAT T	GGGCTATCTCT GAATGTTAAT A	TCAACTTCTGTCGATCTAATTTgaatgtgctgactgctttagatgaagacaaatctcaaaa ctctagctggccttatctactgact/g c gtgctgagagctgctccagcagcagcagctggt cctatggctgctgctgggaagagagatgccgaataattgattgattctcttccaaagatga agttctctcagcttcaaaatgaagactgattgattgattcaatttaactatATTAAACATTGAG GATAGCCCC

FIG. 5WWW

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Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
GNRHu 2	GNRIIR	C	T	F	F	cds	GE569	GGAACACACCA TTTCACTTCT	CAAGGCTTAT CCACTCTTA	GGAAACACCATTTTCATTCTTctctccatctcaaaagctccatctctctctcagatagtc aaagaggttggccaactggcagaaacacgcgtt c/t gaatgcaccacgcacccagccgctt ctccctccgagacctgaagagcgtcgtgaagttaaagtgatcatacatgatcacagcatag agctctAGAGGTGGATAAGCCCTTG
GNRHu 3	GNRIIR	A	C	-	-	noncoding	GE578	CATTAAAGGGC TTTATGTGAGG AT	TCTAAAGAAGA AAAACCTCGTC TA	CATTAAAGGGCTTTATGTGAGGATTTTaaatatacattataaaaaaaagcatagtcatt tgcatataatttaccagcagaaagatttcaatgtctctggaaatattcctataaaaaagaaaga taggaaacagaaagaglcacagactcaactctcaaggagat.tgggatctcttcttggctct ctgctctcaaacaggtaaj a/c agggcttggatatttctACACGAGTTTTTCTTCTTTAGA
GNRHu 4	GNRIIR	C	A	S	Y	cds	GE599	TCAACCTTGTG TGGATCTAATT T	GGGGCTATCCT GAATGTTTAAT A	TCAACCTTGTGCTGGATCTAAATTTgatlgcattctatgctctagaatgaagccatcca ctcclagctggcccllatctactgacttggctggagaggtgct c/a cagccagcactgg cttatggactggccctggagaaagagatgccgaaatttgattgatctctccaagag g/t ta agttctctcagcttcaaaaataagacatagtgattgattccaatttaactaTATTAAACATTCAG GATAGCCCC
GNRHu 5	GNRIIR	G	T	-	-	noncoding	GE599	TCAACCTTGTG TGGATCTAATT T	GGGGCTATCCT GAATGTTTAAT A	TCAACCTTGTGCTGGATCTAAATTTgatlgcattctatgctctagaatgaagccatcca ctcclagctggcccllatctactgacttggctggagaggtgct c/a cagccagcactgg cttatggactggccctggagaaagagatgccgaaatttgattgatctctccaagag g/t ta agttctctcagcttcaaaaataagacatagtgattgattccaatttaactaTATTAAACATTCAG GATAGCCCC
GPIBa 2	GPIBA	C	T	T	M	cds	GE493	CTTCCAGGGGA TGCAGG	AAAGCAAAAG GCAGGAGGT	CTTCCAGGGGATGACAGGGGatccactcaagggtctctctgccacaggctctctctctc ctcttgctctctgctgcacagcccttaccaccccccacccatctgtgaggtctcccaagtgpc cagccactagaagtgaaactgtgacagaggaatctgcagagcgtgcctccagacctgcgnaag acacacccatctctccactgagtagaactctctgtacacctctctctccgcaacctgagct taactctgctcactcagctgaactagatagtgagagctcaccacgtccagctcgatggagc gtgcagtgctggggaccctggatctatcccaactcagctgcaagctcccttgcctgtaggac agacactgctgctctcaccgtctctgagcgtctctctcaacggctgacctgctctggt gacctggtggtcttggcgaactccaagagctctactgaaggccaatgagctgaagacctg cccagggctctga c/t gccacacacacagctggagagctcagctctggctgaacacacactg actgagctcccccgtgggtctctgaatgggctggagaaatctcgacacctctctcccaagaa ctcgtgtatacaatatacaagggtcttcttgggtccccACCCTCTGCTTTTCTTTT
GPIBa 3	GPIBA	C	T	N	N	cds	GE495	GACACCTTCT CCTCCAAGA	GATTGGGTGG GCTCCG	GACACCTTCTCTCTCAAGAGaactcgtctatacaataccaagggtcttcttgggtccacact ctgctcttctgctcttctctccaggaacccctggttatgcaactgtgagatctctatctctc gtggctgcaggacaatgctgaataatgctctacatgttggaagcaaggtgtggagctcaagccatg acctctaa c/t tgggccagtggtgcagtgtaacatccagacaagttctccgtctacaatacc caggaaggggtgcgccccccttggtagagagtgacacagacctatgatatactaccagaa gaggacactgaggggcgaataggtgctgcccacagagctgtggtcaagtctcccaacaaagcca tacaacccctgggtctatctactggtccactgctctctagacagcgaatgacctct cttgatccaacacaaagaa ccactaaggagcagaccacatctccacactagatggaccccaat ttcacactcacatggatctcacatctccaaactccaaactccactactgaacccaccc aagcccgacacctcagagccgtctccggagccgcgcccaaacatgacacccctggagccaccc caagccgacacacccagagccacctcagagcccccagcccccagcccccCGGAGCCACC CCAAATC

FIG. 5XXX

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
GP1Bd4	GP1BA	A	G	R	R	cds	GE495	GACACCTTCT CTTCCAAGA	GATTGGGTGG GCTCCG	GACACCTTCTCTCCACAGAGaactcgtctgatacaataccaagaagggcttttttgggtcccacctctgctcttgccttttccacgggaacccctgggtatgcaactgtagatctctatcttcgtcgtggtcgaagcaatgctgaagaatgctgaaggaagcagggtgtagcctcaagccatgacctcaacgtggcagtgctcagtgacaaatctcagcaaaagtctccgtctcaaaatcccaggaaaggggtgccacccttggtagaagtgacacagacctatgattactaccacagaagggacctgagggcgataaaggtgctgcacaaagactggtgtcaagttcccacaaagccctatacacctggggtctattctactatggctccactggtttctgagacagccaaatgctctctctgcatccaacagaagatccactaaggagcaccacattcccacctag [a/g]ggagcccaaatgtcacacttcacatggaatccatcacattctccaaaactccaaaatccactactggaacaccccgaagccgaccacctcagagccgttccggagccgcctccaaatcagaccacctctggagccacctccaagccaccacccacagacccactcagagccgcgcgcacccagccacccCGAGCCACCCCAATC	721
GP1BA1	GP1BA	G	A	R	H	cds	GE493	CTTCCAGGGGA TGCAGG	AAAGCAAAAG GCAGGAGT	CTTCCAGGGGATCCAGGGgaatccactcaagggctcccttgcgccacaggtctcatgctctctctctgctcgtcgtcgaagcccttacccccaccctctgtgaggtctccaaagtgcagccactagaagtgaaactgtgacaaggaatctgacagcgtgctctccagacctgcgcaagacacacacctccacctggtagaacctctgtacacttctctccacaccttgatgctttacact [g/a]ctcactcagctgaacctagataggtgtagctcgaactcacaagctccaggttcgattgacact [g/a]ctcactcagctgggaccctggatctatcccaaatcagctgcaaaagctgaccttgcctggacagacactgcctgctctcaccgtctggagctctctctcaaccggctgaacctgctccttgggtccctgctggttctgggaactccaaagactctactgaaaggaacatgagctggaagacccctgccccagggctctgacccaccccaagctggagagctcagttcgtctgctgaacacacacttgcagctgagctcccgctgggtctctggaatgggtggagaatctgcacacctctctcctcgaagaaactgcgtgtagatacaataccaagggcttttttgggtcccACCCTCTGACCTTTTGTCTT	708
GP5d1	GP5	C	T	P	P	cds	GE908	AGTACAGGCGC GAAGCT	AACCCCTTGGG CAGGTG	AGTACAGGCGCAACCGTctctgtgtgtgaccacactcccacgttgccttttccagacatgtcgaagggactactgtgcagcgtgctcgggtctctgcgcgccagccttcccctgtccgcagcttgcaagtgtgtcttcggagccgcgcgcagtgctcggggggcgaactggcgcgcatctcgcgctggcctgccacacacctccacacactctctgtcttggaaatggggcgagcgtctctgcagagccagagcttcagcggaatgctcgtgcgcgctcatgtctcgaagccacatctccgcggtgccccc [c/t]ggcaccttcagctgataaaactgaaacacctgaggtgtctgcgcgaacaaatactcagcacttccaggtgcgtctggataaagatggtgctctggagcagttgtttttggaccacaaatgcgtaaggggcattgacaaaacatgttccagaactgggttaeactcggagagcgtcgtctgaaccgaatccagctcgattctctctcgcagctctcttcacgaatctgggaacaccttggttggatattatcggggaacacacctgaccCACCTGCCCCAAGGGGTT	628
GP5d2	GP5	G	A	Q	Q	cds	GE908	AGTACAGGCGC GAAGCT	AACCCCTTGGG CAGGTG	AGTACAGGCGCAACCGTctctgtgtgtgaccacactcccacgttgccttttccagacatgtcgaagggactactgtgcagcgtgctcgggtctctgcgcgccagccttcccctgtccgcagcttgcaagtgtgtcttcgggagccgcgcgcagtgctcggggggcgaactggcgcgcatctcgcgctggcctgccacacacctccacgacactcgtctcttctggaaatggggcgagcgtctctgcagagccagagcttcagcggaatgacgtctcgtgcgcgctcatgattctccgagccacatcttccgcggtgcccccgcaccttcagtgacctgataaaactgaaacacctgaggtgcgcgcaacaaatcacgactctccaggtgcgtctggataaagatgggtgctctggagcagttgttttggaccacaaatgcgttaaggggcattgacaaaacatgttccagaactgggttaacctgca [a/g]agactcgtctcgaaccgaatccagctcgattctctctcgcagctctcttcacgaatctgggaacaccttggaagttgttgaattatcggggaacacacctgaccCACCTGCCCCAAGGGGTT	628

FIG. 5YYY

[illegible]

FIG. 5AAAA

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
GRIN1	GRIN1	G	C	E	Q	cds	GE1287	GAGCTGAGAGAGACTGCGG AGACTGCCG	GTAGGTGCCGG CGGTAACT	GAGCTGAGAGAGACTGCGGctgggcagccttaggtcggtgggtccaggctgggtctccctctc ccccccagattgtgcagatccacag/g/clagcccttcgtatcagtcacgaagccagctgcagtgga tggagacatgcaggaggaggttcacagtcaggcgaccacagtcgaagaagtgatctgcagccgggc ccaacgacgctgcgcgggcagcgtgagtcgcggggcagggcgcggggcggcggggcggcgaggcgc ggggcggtggggcggtctggagccagcagcttTACCgCGCCGCCACCTAC
GRIN1	GRIN1	T	G	C	G	cds	GE1287	GAGCTGAGAGAGACTGCGG AGACTGCCG	GTAGGTGCCGG CGGTAACT	ccccccagattgtgcagatccacagagccttaggttcagtcgaagccacagctgcagtgatcggg aca/t/glcaaggaggaggttcacagtcaggcgaccacagtcgaagaagtgatctgcagccggccca ccaacgacgctgcgcgggcagcgtgagtcgcggggcagggcgcggggcggcggggcggcgaggcgc ggggcggtggggcggtctggagccagcagctTACCgCGCCGCCACCTAC
GRIN1	GRIN1	G	C	D	H	cds	GE1287	GAGCTGAGAGAGACTGCGG AGACTGCCG	GTAGGTGCCGG CGGTAACT	ccccccagattgtgcagatccacagagccttcgttcagtcgaagccagctgcagtgatcggt acatgcaggagaggttcacagtcaggcgaccacagtcgaagaagtgatctgcagccggccca c/g/clacacgctgcgcgggcagccttaggtgcgggggcagggcgcggggcgggggcgggggcgggc ggggcggtggggcggtctggagccagcagctTACCgCGCCGCCACCTAC
GRIN1	GRIN1	G	A	K	K	cds	GE1115	CGCGGAGCTGG GAGGAC	AGGACGCCAG GTGACG	CGCGGAGCTGGGAGGACgctgctgcagtcgcccgcgcgtctgcgctcgaggtgaacacagc acaagaaggaggttgaaattggagatgaaggcgagctgcagtcggcgagcagcagcagcagcagc gcccataaccataaacacagcgcgcgagcagtcacatcgagtttccaagccctccaagtcacagg gctgagctattctgtlcaa/g/a/aggtggggcaggggcggggtggcggggtggcgggcgggggga gtcctggaggggcgggcgcgctGAGCTGCTGCTCCT
GRIN1	GRIN1	G	A	E	E	cds	GE1120	TTCCGGCAGTG GGAGGC	CGTCTCGACC TCGGCT	TTCCGGCAGTGAGGAGCGCGggg/gggaggggggggtcccccggggtccaccttcagccacacgtgcccc cgctcccgagagcagtcacgtgagcttcctgcgcagcgtgcgctctactccacacagtcagtcagc cggtggtttgagatgagtcggtcttcacagctggaaacacatcctctgctggtcagcgacgacc acga/g/a/ggcgggagcctcagaaacgctgctggagagcgtgctggagagcgtgagtcacaggt gggggtcgggcgggcggggtggggcgctgggggAGCGGAGCTGCGGAGCG
GRIL17	GRL	G	T	-	-	noncoding	GE1196	ATTCAAGCTGG CCAAATTAT	AAGAAACAA AAMATGTCC	ATTCAAGCTGGCCAAATTATTtggtaatagaagaatgaaatctaatattaaaatttggaact tctaataattttatatttagttagttagtttcagataataataataataatattgtaattcactactctgg gaagggaggaggtactgcagctttcacagcaattattttaaagattgtaaaatagttctgtgtatag tgcaaaataaggaatgatttttagatgagattgtttatcargacatgttatataatttttggagg g/t/gtcaagaagaatgctgagataacataatgattatgatttggtaagtttgcacatcatctacag cgagcgtggtctcagaacacacacagtttgccttaggggaaggagagtgaggagtcgtccg tgtcagtgaaaggttgtcagggcttcgaccagtgagtcacaggaagtttacttctgtcctcc cttctgcacaccttcacttccacagtgagctctgcagcgaggtttagtttactcaatctc ccttgcactaaagatgtcaagtatgaacaggagacaggaagtggtgtacatccttaaa ggccacatcctaagcgggttacttccatacagcctccccccagcttgaatggacacagaa ggttcagaagtttgcaatagtttgcataagagtcacagcaatattgaatagtgagagatctcca taggttgcaataataactaatcttctatctctacacagagtttattttccaaataaaatg aggacattgtttttgttttctt
GRIL18	GRL	G	T	-	-	noncoding	GE628	GACTTCCCAT TACAGT-TAT TC	GAAGAAACAC AAGGTTTATA TAGTTCC	GACTTCCCATTACAGTTCATTTCctatgtattt/g/ttttaataaccacagctcgaaataaa agaaaaataaagaagatctcagcgagcttcacagagcttcacagaacactctgaaatctct ggtaacaaaaaatagttctcgtcagcgttaccacactcaccctcctggtgcactctgttga ggttatgaaacctgaagtggtatgcaggatataatagctcgttccagacacttagaggga tcatcagctacgtcaacatgtttagggggcggaagtgatggcagctggaatggggcgaaggca ataccaggtgaagtcgaacataaagaGCAACTATATAAACCTTTGTTGTTTCTTC

FIG. 5B BBB

[illegible]

FIG. 5CCC

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[illegible]

FIG. 5DDDD

[illegible]

FIG. 5E EEE

FIG. 5FFFF

FIG. 5GGGG

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
HSU3B2 d28	HSU3B2	C	G	-	-	noncoding	GE665	CTGCTGGGAAA TAGTGAGCTTC	GCTCTTTTGT TGAACCTGTGTG AA	CTGCTGGGAAAATAGTGAGCTTCctactcagcccaattacacctatcaacccccctcaacgcgc 627 acacagtcacattatcaaatagcgtatccactctctctacagaagagctcagcagatctggcg tataagcactctcagcgtgggaggaagcaagcaaaaacccgtggagtgggttgggttcccttgt ggaccgpcacagagagaccctcagtcgaagactcagtgatttaagatgacagagatgtgcagt tgggtatgttaggaatgtcatcaactcaccacactggctctacacagaagcaagagggc aaagcccggtgctgctgctcccttccacaaatgccaaactactgtatctctcatgctc aaaactgcagctcactggcccaacaaagacgtttctgctcctaatcatcacagaagaagaaac aataatattgctgttaccaaatctcagtagctgattctgaacattggaggaccctttaaactg aaggggcccttttgactaatagagctccattccact[c/g]ttaaagtgaagaagcatttcccttc tctttaaactcccttccctTCACACAGTTTCACAAAAGAGC
HSU3B2 d29	HSU3B2	C	T	-	-	noncoding	GE665	CTGCTGGGAAA TAGTGAGCTTC	GCTCTTTTGT TGAACCTGTGTG AA	CTGCTGGGAAAATAGTGAGCTTCctactcagcccaattacacctatcaacccccctcaacgcgc 627 acacagtcacattatcaaatagcgtatccactctctctacagaagagctcagcagatctggcg tataagcactctcagcgtgggaggaagcaagcaaaaacccgtggagtgggttgggttcccttgt ggaccgpcacagagagaccctcagtcgaagactcagtgatttaagatgacagagatgtgcagt tgggtatgttaggaatgtcatcaactcaccacactggctctacacagaagcaagagggc aaagcccggtgctgctgctcccttccacaaatgccaaactactgtatctctcatgctc aaaactgcagctcactggcccaacaaagacgtttctgctcctaatcatcacagaagaagaaac aataatattgctgttaccaaatctcagtagctgattctgaacattggaggaccctttaaactg aaggggcccttttgactaatagagctccattccact[c/g]ttaaagtgaagaagcatttcccttc tctttaaactcccttccctTCACACAGTTTCACAAAAGAGC
HSU3B2 u1	HSU3B2	C	G	R	R	cds	GE639	AAATATAGGCA TCTGCTGAGTG TAT	CCATGCAGAGT TTAAGATGGAG	AAATATAGGCAATCTGCTGAGTGATAaacatttaccctctgttttagccctctctctgggtccac 338 gctagaatcagatctgctctccagcatcttctgttctctggcgaaggtttccctgctactctggat tgccacagatgacggctggagctgctctgtgacagcagcagcaggggtcttctgggtcagagatc gtccg[c/g]ctgtgtgtggagagaggaactgaagagatcagggcccttggacaagagcttca gaccagaattgagagaggaattttcttagtaagtgaacttgagtcagtggttggctggcTCACACTT
HSU3B2 u10	HSU3B2	A	G	-	-	noncoding	GE665	CTCTCTGGAAA TAGTGAGCTTC	GCTCTTTTGT TGAACCTGTGTG AA	CTGCTGGGAAAATAGTGAGCTTCctactcagcccaattacacctatcaacccccctcaacgcgc 627 acacagtcacattatcaaatagcgtatccactctctctacagaagagctcagcagatctggcg tataagcactctcagcgtgggaggaagcaagcaaaaacccgtggagtgggttgggttcccttgt ggaccgpcacagagagaccctcagtcgaagactcagtgatttaagatgacagagatgtgcagt tgggtatgttaggaatgtcatcaactcaccacactggctctacacagaagcaagagggc aaagcccggtgctgctgctcccttccacaaatgccaaactactgtatctctcatgctc aaaactgcagctcactggcccaacaaagacgtttctgctcctaatcatcacagaagaagaaac aataatattgctgttaccaaatctcagtagctgattctgaacattggaggaccctttaaactg aaggggcccttttgactaatagagctccattccact[c/g]ttaaagtgaagaagcatttcccttc tctttaaactcccttccctTCACACAGTTTCACAAAAGAGC

FIG. 51111

FIG. 5JJJJ

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
HSD3B2 u15	HSD3B 2	C	T	-	-	noncoding	GE665	CTGCTGGAATAGTGAGCTTC TAGTGAGCTTC	GCTCTTTTGT TGAACGTGTG AA	CTGCTGGAATAGTGAGCTTCtactcagcccaatttaccctctacaaccccccttcaacgccc acacagtcacattatcaaatagcgtcttaccctctcttacaagaagctcagcagatctggcg tataagccacttacagctgggaggaagcagcagcaaacctggagtggttggctctctgt ggaccgacagaaggaacctgaagctccaagactcagtttaaggatgacagagatgctgatg tgggtattgttaggaatgtcatcaactccaccctggctctacacagaaatgctctcatgctc acaagccaggctcgtgctcccttccacaatgcccaacttactgtattctctcatgctc aaaalcttctgacagctactgcccacaacaagaagctttctgctctaatcatcacagaagaa aaacaatattgttctgttaccaaatctcagtagctattcttgaaacaaatgagggacccttaa actgaaggcccttttgactaatagagctccatttccactcttaaatgagaagcatttcccttc tccttaactctccattcttcacacacagcttcaacaaaagagc
HSD3B2 u16	HSD3B 2	A	C	-	-	noncoding	GE665	CTGCTGGAATAGTGAGCTTC TAGTGAGCTTC	GCTCTTTTGT TGAACGTGTG AA	CTGCTGGAATAGTGAGCTTCtactcagcccaatttaccctctacaaccccccttcaacgccc acacagtcacattatcaaatagcgtcttaccctctcttacaagaagctcagcagatctggcg tataagccacttacagctgggaggaagcagcagcaaacctggagtggttggctctctgt ggaccgacagaaggaacctgaagctccaagctcagtttaaggatgacagagatgctgatg tgggtattgttaggaatgtcatcaactccaccctggctctacacagaaatgctctcatgctc acaagccaggctcgtgctcccttccacaatgcccaacttactgtattctctcatgctc aaaalcttctgacagctactgcccacaacaagaagctttctgctctaatcatcacagaagaa aaacaatattgttctgttaccaaatctcagtagctattcttgaaacaaatgagggacccttaa actgaaggcccttttgactaatagagctccatttccactcttaaatgagaagcatttcccttc tccttaactctccattcttcacacacagcttcaacaaaagagc
HSD3B2 u17	HSD3B 2	G	T	L	L	cds	GE1194	CACAGAATGCG ACCCTGAGTC	GCAGATCTCG CTGAGCC	CAGAAGAATGCGACCTCGAGTTCataacacacacacagcagggagggaggggacacacagc gcccagcaglygagcagcctcgggagaaatctctcaacacacacacacacacacacacacacac taccagctacttg/tctggggcctgtgttccagccagctgtgcccagctctctctacacacag agctagaaggtagcggcccaactctcaaggaatctctcagcagcagcagcagcagcagcagc tctggaacacacatggccacactcaccctacagcaaaaagcttgcctgagagagctgtgctg cggctaatgggtggaatctaaaaatggatgacttctgacttggcttgaagacacacacacac atctatgggagagggagggccactctctctgcccagtaaatgagggcctgaacaacatgggat cctgcagtggtggaaagtctccacagcaacccagctctatgttggaacagtggtggtggccc acattctggccttgaggccctcagaccacacacacacacacacacacacacacacacacac taccctcagatgacagcctcaccacacacacacacacacacacacacacacacacacacac ggggctcagcttgagcttctcactcagcccaatttaccctctacaaccccccttcaacgccc gtcacattatcaaatagcgtcttaccctctcttacaagaagccttcaaccccccttcaacgccc
HSD3B2 u18	HSD3B 2	C	T	L	L	cds	GE665	CTGCTGGAATAGTGAGCTTC TAGTGAGCTTC	GCTCTTTTGT TGAACGTGTG AA	CTGCTGGAATAGTGAGCTTCtactcagcccaatttaccctctacaaccccccttcaacgccc acacagtcacattatcaaatagcgtcttaccctctcttacaagaagctcagcagatctggcg tataagccacttacagctgggaggaagcagcagcaaacctggagtggttggctctctgt gggtataagccacttacagctgggaggaagcagcagcaaacctggagtggttggctctctgt tcttgaccgacagaaggaacctgaagctccaagctcagtttaaggatgacagagatgctgatg catgtgggtattgttaggaatgtctcaactccaccctggctctacacagaaatgctctcatg gggacagaagccaggtctgctgctcccttccacaatgcccaacttactgtattctctcatg catcaaacctcagcagctcactggcccacaagaagctttctgctctaatcatcacagaagaa aaacaatattgttctgttaccaaatctcagtagctattcttgaaacaaatgagggacccttaa actgaaggcccttttgactaatagagctccatttccactcttaaatgagaagcatttcccttc tccttaactctccattcttcacacacagcttcaacaaaagagc

FIG. 5KKKK

[illegible]

FIG. 5L1LL

[illegible]

FIG. 5MMM

[illegible]

FIG. 5NNNN

[illegible]

FIG. 50000

FIG. 5PPPP

[illegible]

FIG. 5Q

[illegible]

FIG. 5RRRR

103/178

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
HTR1Du 11	HTR1D	C	A	A	D	cds	GE1162	TTGAAGGAAGG AGCCAAATG	TGTAGAGATC TGAGAGGTGTT CA	TTGAAGGAAGGAGCCAAATGtctgtggaggtctgtgggaagagagagccacccatagcatgtcccact gaaccagtccagcagaagccctcccagaggagccctccacagatccctgaatgccacagaacct cagaggtctggagatcccaggagccctccagggagccctccagatcccttccgtggctcttcgttc atcacactggccacagtcctctccaatggcttctgtactcaccacatcttactcaccaggaagt ccacacctgccaaactacctgattggctcctccgcccaccacccctcttggtttccatctgg taatgccatcagcatcgtctataccatcaccacacccctggaaacttggccaatcttctgtgac atctgggtctctctgacatcagtgctgcacagccctccatcctgcactctctgtcatgtctt ggcagggtctgggcaatcacagatgccctggaaatcacgtaaacacagagagggctggccacgg ccaccatgatcgccattgtctgggcatctccatctgcatctccatccccctctctctggcgg caggccaagg [c/a]ccaggaggagatgtcggactgtctggTCACACCTCTCAGATCTCTACA	650
HTR1Du 2	HTR1D	T	C	II	H	cds	GE1162	TTGAAGGAAGG AGCCAAATG	TGTAGAGATC TGAGAGGTGTT CA	TTGAAGGAAGGAGCCAAATGtctgtggaggtctgtgggaagagagagccacccatagcatgtcccact gaaccagtccagcagaagccctcccagaggagccctccacagatccctgaatgccacagaacct cagaggtctggagatcccaggagccctccagggagccctccagatcccttccgtggctcttcgttc atcacactggccacagtcctctccaatggcttctgtactcaccacatcttactcaccaggaagt ccacacctgccaaactacctgattggctcctccgcccaccacccctcttggtttccatctgg taatgccatcagcatcgtctataccatcaccacacccctggaaacttggccaatcttctgtgac atctgggtctctctgacatcagtgctgcacagccctccatcctgcat [c/t]ctctgtgcatgtg ctctggacaggtactgggcaatcagatgccctggaaatcacgtaaacacagagagggctggccac gcggccacatgatcgccattgtctgggcatctccatctgcatctccatccccctctctctgtg gcggcaggcccaaggcccgaggagatgtcggactgtctggTCACACCTCTCAGATCTCTACA	650
HTR1Du 3	HTR1D	T	C	A	A	cds	GE1162	TTGAAGGAAGG AGCCAAATG	TGTAGAGATC TGAGAGGTGTT CA	TTGAAGGAAGGAGCCAAATGtctgtggaggtctgtgggaagagagagccacccatagcatgtcccact gaaccagtccagcagaagccctcccagaggagccctccacagatccctgaatgccacagaacct cagaggtctggagatcccaggagccctccagggagccctccagatcccttccgtggctcttcgttc atcacactggccacagtcctctccaatggcttctgtactcaccacatcttactcaccaggaagt ccacacctgccaaactacctgattggctcctccgcccaccacccctcttggtttccatctgg taatgccatcagcatcgtctataccatcaccacacccctggaaacttggccaatcttctgtgac atctgggtctctctgacatcagtgctgcacagccctccatcctgcatctctgtgcatgtc [t/ c]ctgagacaggtactgggcaatcagatgccctggaaatcacgtaaacacagagagggctggccac gcggccacatgatcgccattgtctgggcatctccatctgcatctccatccccctctctctgtg gcggcaggcccaaggcccgaggagatgtcggactgtctggTGAACCTCTCAGATCTCTACA	650
HTR1Du 4	HTR1D	T	C	N	N	cds	GE1161	AGGAGGAGATG TCGGACTGT	ATCCCGATGAG GTTACAGGA	AGGAGGAGATGTGCGACTGTcttggtagaacctctcagatctctacacatctactccactgt ggggcttctacatctccctgggtgtgctcatctatattggcggatctccgggtgcccgt gaaccgcatctgtaatccacccctcaactctatgggaagcgtccaccagccaccctcatcacag gctctgccgggtctcgtctcgtctcgtctcaactcagcctccatcaggggagctcgcactcggct ggctccctctcttttcaaccacgtgaataatcagcttgcagcagtgccctgggaacagag gattctgctgctcgaagaaggaaagcccaaaatcctgggcatcttctgggggctcttaca tctgctgggtgctctctctggtgtctcttggctcccatctcctgggagctctcctgtggatc caccggcgtcttctgactctcactgggtaggtctttaaactccctcatcaatcccaat ccactgtgtttaa [c/a]gaagaggtctggcagagcttttcagaaaattgccccttcgggaag gctcctcagttctattcgtgtgacgcagaaagaaacttttgtTCTCTTAACCTCTATCGGGAT	648

FIG. 5TTTT

[illegible]

FIG. 5UUUU

[illegible]

FIG. 5VVV

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
HTRIEL _L	HTRIE _L	A	T	E	V	cds	GE1160	TTCCCTTGTGTA CAGGTATCCAT	GTGGGATGTAG AAGCTCCA	TTCCCTTGTGTACAGGTATCCATTTtccagctctataatactctttaaacaagaagaalggattctt ttaaattcatctgatacaaaattgacctcagagaaactgtaaacagaatgccaacaaattct gggtgccctcactctgtctggctggcactgatgacaaacactatacaactcctgtgacgcgtg caattattgtgaccgggaagctgcacacccagccaattatttaattgtctcccttgcagtcacac gattctcttggctgtccctggatgcccttcagcattgtatatttggagagagagctgggat tatggggcaagtgtgtgacatttggctgagtttggacttacctgtgcacgtgcacgtcccatct tgcattctcagctatagcttggatcggatcagcaaatcagcagatcgtctgtg/ttjglatcc caggaagaagactccaaagcatgctggcatttatgattacaatagtttggatatactctgtttta tctctatgctctctatcttggaggccaaggaactgagcagatgatggaatgacatcatcaag cagcaccaattgttctccaccatttactcaacatttggagccttcttgcattccccctgcattgatt CGACCACATGTGTTCACCATtactcaacatttggagccttcttgcattccccctgcattgatt tgaattcttactcaaaaatatagcagcagaagaactatataccacaagcagcagaagtagg attgcaaggagaggtgaattggccagtccttttggagatggttgagaagaagcactaaactcag ttccacatctatgtactagaagaattcttacttgcaccatcaacagacttgcataaaat [c/a] catagcacagtgagaaggtctcggctgtaattcaagcatgagaatacttgggaagggcacaagat ctcaggtcacaagagcgggaagcagccactccttgggatttaattcttgggtgcaatttgaatat gttggctctctttttttaaagaatttggtttaattctgtgacaagaatgaaaatttctgaa gaaatgtccaatttttggcatgcttgggttctcaattccttcaataatcactcatttctacac aatctttaatgaagacttcaagaagaacttccaaagccttggcggatgtgcagttgattgtttaa aatgtttatttggaggattgggggttttggaggcaggaatTAAT	640
HTRIEL _{u5}	HTRIE _L	T	A	I	I	cds	GE1158	CGACCACATTC TTTCCACCA	AGTTATTCCTC CCCTCAAAA	CGACCACATGTGTTCACCATtactcaacatttggagccttcttgcattccccctgcattgatt tgaattcttactcaaaaatatagcagcagaagaactatataccacaagcagcagaagtagg attgcaaggagaggtgaattggccagtccttttggagatggttgagaagaagcactaaactcag ttccacatctatgtactagaagaattcttacttgcaccatcaacagacttgcataaaat [c/a] catagcacagtgagaaggtctcggctgtaattcaagcatgagaatacttgggaagggcacaagat ctcaggtcacaagagcgggaagcagccactccttgggatttaattcttgggtgcaatttgaatat gttggctctctttttttaaagaatttggtttaattctgtgacaagaatgaaaatttctgaa gaaatgtccaatttttggcatgcttgggttctcaattccttcaataatcactcatttctacac aatctttaatgaagacttcaagaagaacttccaaagccttggcggatgtgcagttgattgtttaa aatgtttatttggaggattgggggttttggaggcaggaatTAAT	631
HTRIEL _{u6}	HTRIE _L	T	G	D	E	cds	GE1160	TTCCCTTGTGTA CAGGTATCCAT	GTGGGATGTAG AAGCTCCA	TTCCCTTGTGTACAGGTATCCATtctcagctctataatactctttaaacaagaagaagaattgattct ttaaattcatctgatacaaaattgacctcagagaaactgtaaacagaatgccaacaaattct gggtgccctcactctgtctggctggcactgatgacaaacactatacaactccttggatcgcgtg caattattgtgaccgggaagctgcacacccagccaattatttaattgtctcccttgcagtcacac gatttcttggctgtccctggatgcccttcagcattgtatatttggagagagagcctggat tatggggcaagtgtgtgacatttggctgagtttggacttacctgtgcacgtgcacgtcccatct tgcattctcagctatagcttggatcggatcagcaaatcagcagatcgtctgtgagatggccagg aaaaggactccaaagcatgctggcattatgattacaatagtttggatttatctgttttctctc tatgctcctctatctctggaggccaaggaactcagagatgatt/gjuaatgcattcatcaag cagcaccaacttgttctccaccatttactcaacatttggagccttcttgcattccccctgcattgatt CAGCCAAAGGMAATAACCAACagcttctccacagttgaaactgaaacaaggaagaacatggaacat cacaacatgtaccagaagggccagcatggctataaagcccaagcactcatcagtagaagatgctca tttgcattgacttgggtgtcttccacctccaccttgcacttgcacttgccttgcctgtgattc/ci ggctatttggcaccacaagaagctccacagcttgcacactactacttcttcttctggccgtg cggacctcctgtggcagttgctcactgcccctgagcactcatcactatgtcatggatcgtctg aagcttgggttaattctctgtgagggttggctgagttggacatgacctgtgcacctgtccat cctccacctctgtctatggcctggagcaggtactgggacctcaccacagctatggaatgccca gggaaggagcggccaaagggccgctgattcttacccttctgtgacattgacatttcttccat tccatgccccctctgtcttgagaagccacggcgcctaaagcctcccccttagtcagtcacat cccaagccacacacatttactcaacatttggagccttcttgcattccccctgcattgatt cccaagccacacacatttactcaacatttggagccttcttgcattccccctgcattgatt	640
HTRIEL _{u1}	HTRIE _L	T	C	I	T	cds	GE1157	CAGCCAAAGGA AAATACCAA	GCACCCAGCGT GGAGTAAT	CAGCCAAAGGMAATAACCAACagcttctccacagttgaaactgaaacaaggaagaacatggaacat cacaacatgtaccagaagggccagcatggctataaagcccaagcactcatcagtagaagatgctca tttgcattgacttgggtgtcttccacctccaccttgcacttgcacttgccttgcctgtgattc/ci ggctatttggcaccacaagaagctccacagcttgcacactactacttcttcttctggccgtg cggacctcctgtggcagttgctcactgcccctgagcactcatcactatgtcatggatcgtctg aagcttgggttaattctctgtgagggttggctgagttggacatgacctgtgcacctgtccat cctccacctctgtctatggcctggagcaggtactgggacctcaccacagctatggaatgccca gggaaggagcggccaaagggccgctgattcttacccttctgtgacattgacatttcttccat tccatgccccctctgtcttgagaagccacggcgcctaaagcctcccccttagtcagtcacat cccaagccacacacatttactcaacatttggagccttcttgcattccccctgcattgatt	630

FIG. 5W WWW

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
HTRIEU 2	HTRIE	G	T	E	D	cds	GE1156	GCACGACCATG TTATCTACACC	CCCATCCATCTC ATGAGGCT	GCACGACCATGTTATCTACACCATtactccacgctgggtgcgtttatatcccccttgactttga tactgattctctattaccggatttaccacggcccaagcctttaccagaaaggggatacaagtt cggccttaagcaagaagcacagatagccagaattcttttgcgaattgttgaagttgtaactttacacagac ttctgtgtgtgactctccactcagaccctaccacagatttgaagaagttccatgtctccca tcagatgccccccttcgaatgatcatcaccacgaggaacgctcagcagatcctctagcacc agggaacggaagcagcagatcctgggtgattctgggtgcattcttattctctgctgccc attttctcaaaagagtg/lttgattgtgggtctgaagcatcacacggtgctctcggaagtgccc gactttcagcgtggctcggtttatgtgaattctctgatacaccctctgtctatacagagttttaa tgagaactttaagctggcttttaaaagctcatctagatgcgagagacacttagtagctgaataa gtcaaaagcagcagcttttccagAGCTCTCATGTCGATGGG
HTRIEU 3	HTRIE	C	A	L	I	cds	GE1156	GCACGACCATG TTATCTACACC	CCCATCCATCTC ATGAGGCT	GCACGACCATGTTATCTACACCATtactccacgctgggtgcgtttatatcccccttgactttga tactgattctctattaccggatttaccacggcccaagcctttaccagaaaggggatacaagtt cggccttaagcaagaagcacagatagccagaattcttttgcgaattgttgaagttgtaactttacacagac ttctgtgtgtgactctccactcagaccctaccacagatttgaagaagttccatgtctccca tcagatgccccccttcgaatgatcatcaccacgaggaacgctcagcagatcctctagcacc agggaacggaagcagcagatcctgggtgattctgggtgcattcttattctctgctgccc attttctcaaaagagtg/lttgattgtgggtctgaagcatcacacggtgctctcggaagtgccc gactttcagcgtggctcggtttatgtgaattctctgatacaccctctgtctatacagagttttaa tgagaactttaagctggcttttaaaagctcatctagatgcgagagacacttagtagctgaataa gtcaaaagcagcagcttttccagAGCTCTCATGTCGATGGG
HTRIEU 4	HTRIE	C	T	H	H	cds	GE1157	CAGCCAAAGGA AAATAACCAA	GCACCCAGCGT GGAGTAAT	CAGCCAAAGGAATAATCCACagcgttctccacgttgagactgaacaaaggaagacatgaacat cacaaactgtaccagagggcagcagatggctataagaccacgaaccatcaetggaagagatgctca tttgcagactctgggtgctatcacacccttaccacagtgctgaacttggctgtgatactggct attggcaccacaaagctccacacgctgcacactcaactaatctgttctctggccgtgaacgga cctctgggtggcgtgctgctatgccctggagcatcatatcatgtctatggatcgctggagcga ttgggtacttctctggaggtgggtgagtgagcatgacctgtctgacacgtcccatctctc cagcttctgtctatgccctggcaggtactgggacatgacctgtgacacgtcccatctctc gaggaagcgaagagggcgcgtgatactcttcagctctggaacatcatgaaatcgcacgaaga tgccccctctgtctggagaagacacgcgcgcctaaagcctctccctcctcagtgcaagtgacacg ca/c/l/gaacatgttactccacccATTATCCAGCTCTGGTGGTGC
HTRIEU 5	HTRIE	C	T	S	F	cds	GE1156	GCACGACCATG TTATCTACACC	CCCATCCATCTC ATGAGGCT	GCACGACCATGTTATCTACACCATtactccacgctgggtgcgtttatatcccccttgactttga tactgattctctattaccggatttaccacggcccaagcctttaccagaaaggggatacaagtt cggccttaagcaagaagcacagatagccagaattcttttgcgaattgttgaagttgtaactttacacagac ttctgtgtgtgactctccactcagaccctaccacagatttgaagaagttccatgtctc/1 tctcagagatcccccttcgaatgatcatcaccacgaggaacgctcagcagatcctctag caccaggaagcagagcagcagatcctgggtgattctgggtgcattcttattctctgccc tgccattttctcaaaagagttgattgtgggtctgagcatcacacgtgctctcggaagtgccc gactttctgagcgtggctcggtttatgtgaattctctgatacaccctctgctatacagagttttaa tgagaactttaagctggcttttaaaagctcatctagatgcgagagacacttagtagctgaataa gtcaaaagcagcagcttttccagAGCTCTCATGTCGATGGG

FIG. 5XXXX

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
HTR2ad 14	HTR2A	C	T	-	-	noncoding	GE1167	TGGTACTGCGA AACCA	GCCACTGCTAG GATCCTGTT	TGGTACTGCGAACCACCACTATTCTCTCCACCATGTGGGTTTGAATAATCTGGGTGGCATA TTCTCTGTGAGAAATAAAGCCAGTTCAATGGTGTATCTCTATTAATAATAAATAAGTGTCAATAGTT TATCAGAGTTATCACCACAGACTGCTAGCCACCTGAGCCTATGTGGCAATGTCAATATCC ACTCTGGACACAAACACTGTGGCTTTGGATGGAGTCCAGACACTCAGCACTC/T/GAG GACATACTTTCTTCTAGCTTATTTATGTTCTCTCTCCCTCCAGCTCAAAATACCACAG TGCACTTACTTACTCTTAATGGGAATCTGCAAAAGGCCATTCTCCAGTTCTCTCAAGCA AAGGAAACTTCCCAATATTAATATGTAGCAAAAGGGAGAGAAAGAGCTGTGGTCCGC CCCTCGCTGTGCTACTCTGAGCTTATGACATACATAGAGGGAGGTGTGATGAATGAGC GAGACGTGAGGGAGCTACTCATCCCTGGAAACAGGAGTCCCTTGGTGGACAGCTCTC CTACTTCCCATGTCAGTTCTTTGTGGACTTGGAGGCTGTGAATGATTTCTAAATGTGTC CTGTGAGGCGAGCGCACAGGAGGGAGGCCAGCGAGCGTGTCCAGAGGAGCCAACAGG ATCTTAGCAGTCCG
HTR2ad 15	HTR2A	G	A	-	-	noncoding	GE1169	CCGTGCCAGAG GAAGCC	CTACCAACCC GAGGACAAA	CCGTGCCAGAGAGACCAAGGATCTCTAGCAGTGGCGAGTGGCTCAGCTCTGTGTCAGTCTT TTGAGTCAGAAAACAGAAACCAATTAATCTATCTATCTGTGGTGGAGATCAAGAGAGG GACTTACACCAAGTTTAATCTGTGAGAGATGCGAGTGCAGAGATCAACAATGTATCTCAT GTGTGAACCTGAGAGACAAATGTAGTTCTCTCATGCCCTATATTTATGCTGTGAATTTCTT TCCGGTTGAAATCATGCTTGGCCAACTGTAATCTTCAATGAGAAATCCAGGGGGAGAGT TGCTGTCTATCTTACTAAGACTTTTGTCTCTCTTATAGCTAAGCACTATAGGAG CTGAAATCTGACAGCAGCTGGCAATTCAGCTAAGATGGCTGAGACTGTAACTCAAGAG TACATCAATTAATGATTAACACTGGATTTTCTTAAATGACTTTCTTAAATGTAGATGT GTACATCCCACTGTCTGTGATGCTGCTATTTAATAACTGTGTGCTAACTAGTACCATC G/A/GCATAACCAACAAATGAGATATGTTAAACAAGAGTCCAGTAGTTATAAACTTTCTT CTTGTCCAGAACATTTCTCTCCCGAACCTCAAAACCAACCTGCAACCTCTATGCTAAAG TTCTATCTGTCTTTTGTCTCTGTTGGTGGAG
HTR2au 1	HTR2A	G	C	-	-	noncoding	GE1167	TGGTACTGCGA AACCA	GCCACTGCTAG GATCCTGTT	TGGTACTGCGAACCACCACTATTCTCTCCACCATGTGGGTTTGAATAATCTGGGTGGCATA TTCTCTGTGAGAAATAAAGCCAGTTCAATGGTGTATCTCTATTAATAATAAATAAGTGTCAATAGTT TATCAGAGTTATCACCACAGACTGCTAGCCACCTGAGCCTATGTGGCAATGTCAATATCC TCCACTGTGACACAAACACTGTGGCTTTGGATGGAGTCCAGACACTCAGCACTCAGCTCCGAG GACATACTTTCTTCTAGCTTATTTATGTTCTCTCTCCCTCCAGCTCAAAATACCACAG TGCACTTACTTACTCTTAATGGGAATCTGCAAAAGGCCATTCTCCAGTTCTCTCAAGCA AAGGAAACTTCCCAATATTAATATGTAGCAAAAGGGAGAGAAAGAGCTGTGGTCCGC CCCTCGCTGTGCTACTCTGAGCTTATGACATACATAGAGGGAGGTGTGATGAATGAGC GAGACGTGAGGGAGCTACTCATCCCTGGAAACAGGAGTCCCTTGGTGGACAGCTCTC CTACTTCCCATGTCAGTTCTTTGTGGACTTGGAGGCTGTGAATGATTTCTAAATGTGTC CTGTGAGGCGAGCGCACAGGAGGGAGGCCAGCGAGCGTGTCCAGAGGAGCCAACAGG ATCTTAGCAGTCCG

FIG. 5ZZZZ

[illegible]

FIG. 5A AAAA

[illegible]

FIG. 5CCCC

Poly ID	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
HTR2A 7	HTR2A	A	G	-	-	noncoding	GE1167	TGGTACTGCGCA AACCA	CGCACTGCTAG GATCCTGTT	TGGTACTGCGCAACCAACTatttctccaccatgtgaggttttgaaataataactctgggtggcata ttcttgcgtgaagaaaaaagccaggttcaatgggtgatctatttaataaaaaatagtgtaataatg tatcagaggttatcaccacagactgcttagccacctgagcctatggtccaatgtctcagtttaattcc actctggacacaaacactgttggttttggatggaggtgcagacactcacagctccgagagaca tactgttttctagccttattatgtctcttccaccttccagcttccagctaaaaataaccacagtgcc acttacctacttaattgggaatctgcacaaaagggcatttctccagtttctctcctcaaaagcaagg aaaacttccc[a/g]atataatgttagcaaaaaggagggaagaaaagcctgtttgttccgcg ccctctggctgttgccttctgcagctttagacatacactagaggaggtctgatgaaatgaac ggagacgctcagagagctactccatttcggaaacaggagtcctctgggcagacagctcttc ctacttcccatcagattcttttggagactttggagggctctgtaattgttcttaattgtgtgc ctgctggagggagccgcacaggaggagggaacccagcggagcgtgcccagagggaagccAACAGG ATCCTAGCAGTGCG
HTR2A 8	HTR2A	A	G	-	-	noncoding	GE1167	TGGTACTGCGCA AACCA	CGCACTGCTAG GATCCTGTT	TGGTACTGCGCAACCAACTatttctccaccatgtgaggttttgaaataataactctgggtggcata ttcttgcgtgaagaaaaaagccaggttcaatgggtgatctatttaataaaaaatagtgtaataatg tatcagaggttatcaccacagactgcttagccacctgagcctatggtccaatgtctcagtttaattcc actctggacacaaacactgttggttttggatggaggtgcagacactcacagctccgagagaca tactgttttctagccttattatgtctcttccaccttccagcttccagctaaaaataaccacagtgcc acttacctacttaattgggaatctgcacaaaagggcatttctccagtttctctcctcaaaagcaagg aaaacttcccataataatgttagcaaaaaggagggaagaaaagcctgtttgttccgcctc ctggctgttgcacttgcagcttatgacatacac[a/g]tagaggagggtctgatgaaatggaac ggagacgctcagagagctactccatttcctgtggaacccagggtcccttggctggagacagctcttc ctacttcccatcagcttcttttggcagctttgggggtctgtaattgttcttaattgtgtgc ctgctggagggagccgcacaggaggagggaacccagcggagcgtgcccagagggaagccAACAGG ATCCTAGCAGTGCG
HTR2A 9	HTR2A	G	A	-	-	noncoding	GE1169	CCGTGCGCAGAG GAAOCC	CTCACCAAAC GAGGACAAA	CCGTGCGCAGAGAACCCacaggatcctgacagtgggagctggctcagctcttgcagctgagttt tgagctcagcaaacagaacaaaataactactatcatattgttggtagggagctcagagctcagagat gactctacacaggtttaatctgtaggagtcagagctgcagataacaaagataacaaatgactctcat gttgaaacctgaagacaaatgaagtctctcatgcgcataattttattgctgctgtaattctctt tccggtttgaaatcatgcttggccaaatgaactatttcaatgagaatttccaggaggagaagt tgctgctaatcttacttgaagctttttgtttctcttcttcaatgagaacatacatataggag ctgaaattcttcagcagcgtctggcaattca[a/g]cctaaagatggctggagactgtgaaccca aagatacatccaattactatgggataacactggatgatttttaattgactcttcaattgtatga atgtgctacatccccactgttctgattgcatgctattttaataactgtgtgctaaactagtacc atcgcataaaccaacaaatagatatagtttaaacaaaggtcccagtagttatataaactttcttt cttggccagaacatttacttccccgagcgtcaaaaaaacccgcacactctatagctaaaag tttcaattctgcttttTTTGCTCGTGTGGTAG
HTR2C 11	HTR2C	G	C	S	S	cds	GE1126	TTTTTCAGTGT GCACCTAAATTG	ACTTACATMA AGGATTGCC	TTTTTCAGTGTGCACCTMAATGgctctatgggtggcaat[g/c]gatacttctgtgagccag tagcagctcatagtaactgacatttcaactactccagctgggtgagcgtcttcaattcccgagcggg gtcaaaaactggcagcacttctcaatgcatacaataaataacatgactgagttggcacaatcc tgtgcatcagtcagtaagcatggaagaagaaactgcacaatgcccacaaactacttcaattgctcc tagccattgctgataatgctagtgaggactactgtcatgcccctgctctccctGGCMAATCTTTAT

FIG. 5DDDD

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
HTR2Cu 2	HTR2C	A	C	M	L	cds	GE1275	CCTAGATATT GTGCCCGT	CGATCAAGC AAATGT	CCTAGATATTTGCCCCGCTGGAGTtcttttagatgttttattttcaacagctccatc/a/c/ tgcacctgcgtatatactcgtggatcggatgtagcaatacgtatactctatctgagcatagccgt ttcgaatttcggagactaaggccatcagaagattgctattgtttgggcgaatttctataggtaaatata aaacttttggccataagaattgcagcggtatgctcaatacttcggataatttactgtactgtgaaca acgtacacagcgtcgtggataACATTTCCTTGTATCG
HTR2Cu 3	HTR2C	C	G	L	V	cds	GE993	CAAAGAAAG ATGATATGATG	TTACAGGATG AATGCACCG	CAAAGAAAGATATATGACacttagcgtcgtatcgttggaac/c/g/tgaggaaatgCGGTGATTCATTTCCTGTAA tgccttaagctgaagcaatcatggtgaac/c/g/tgaggaaatgCGGTGATTCATTTCCTGTAA
HTR2Cu 4	HTR2C	C	G	I	M	cds	GE1275	CCTAGATATT GTGCCCGT	CGATCAAGC AAATGT	CCTAGATATTTGCCCCGCTGGAGTtcttttagatgttttattttcaacagctccatc/a/c/ cctctgcctatactcgtggatcggatgtagcaatacgtatactctatctgagcatagccgttcca attcggcactaaggccat/c/g/ataggaattgctattgtttgggcgaatttctataggtaaatata aaacttttggccataagaattgcagcggtatgctcaatacttcggataatttactgtactgtgaaca acgtacacagcgtcgtggataACATTTCCTTGTATCG
HTR5Au 1	HTR5A	T	C	II	H	cds	GE1319	TCTGCAAGTAC CCCAGG	GGATTGCTGAG ATACCCA	TCTGCAAGTATCCCCAGGcggctctcttgaccacagaga/gggatttaccagtagaacctaacctctt tctctcttccacccctcccttttggagacacacagcgtcggcaagagacacttgcctccca gctgcacctctcgtcttcggatgcttattctcaacttctggtgttcttgggtcttcttgggtgcgtgc ccactctggaacctgctggctggagacacatcttcctgtagcagccttccacgcgtgcgc ccaaacctgtggcatccatggtcgtctcggatgctcgtgtggtcgcgtcgtggtcagcgtctga gactggatga/tc/gtagctgtccgggcgcgtcggcagctaggctcggagggctgtgccaagctttg gatcgtgcagctgctctgtgcagcggcagcatctggaaactgacggggcagtagccttcccaagctc gctactgttccatcacgcgcacatggaaatacacgctcgcaccccaagctgcttcccaagctc atgatcgcctcaactgggcactctcctgctcatctcttggcccgctcttcttgggtggggg agagacgtactctgaggcagcagaggtgcgaagtgaaagcgcgccttctcagcgcgtctct ccacgtgaggcgtctcactgcgcgtctgtgtgctgctctcgtgtactggaagatctacaag gctgccaagtctcgcgtgggtccaggagaagcaactagcgtctcaccatactcgaagcgtgtgga ggTGGGTATCTACGCAATTC
HTR5Au 2	HTR5A	A	T	P	P	cds	GE1319	TCTGCAAGTAC CCCAGG	GGATTGCTGAG ATACCCA	TCTGCAAGTATCCCCAGGcggctctcttgaccacagagatggatttacc/a/t/gtgaacctaacct ccttctctctccacccctcccttttggagacacacagcgtcggcaagagacacttgcgtcggc cccaactgcctctcgtctcgtctcggatgcttattctcaacttctggtggcttcttgggtggc ggccagcttgccttgcgaaccttgggtgctgggcacacatctcgtgtgacacacttccaccgcg tggccacaacctggtagcatcctagcgtctcggatgctcgtgtggtcgcgtgggtcagctgctc ctgacctggtagatgactctcgggcgcgtcgtgcagctaggctcggagcgtctgcagcgtttg gatcgtgcgaactgctttgtgcagggcagcatcttgaaactgacggccatagcctgggacc gctactgttccatcacgcgcacatggaaatacacgctcgcaccccaagctgcttcccaagctc atgatcgcctcaactgggcactctcctgctcatctcttggcccgcttcttgggtggggg agagacgtactctgaggcagagtagtcaggtaagcgcgccttctcagcgcgtctct ccacgtgaggcgtctcactgcgcgtctgtgtgctgcttctcgtgtactggaagatctacaag gctgccaagtctcgcgtgggtccaggagaagcaactagcgtctcaccatactcgaagcgtgtgga gctgccaagtctcgcgtgggtccaggagaagcaactagcgtctcaccatactcgaagcgtgtgga gctgccaagtctcgcgtgggtccaggagaagcaactagcgtctcaccatactcgaagcgtgtgga

FIG. 5EEEEE

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
HTR5Au3	HTR5A	C	T	I	I	cds	GE1319	TCGCGAGTAC CCGAGG	GGATTGCTGAG ATACCCA	TTCTGCAAGTACCCAGCGggtctctcagccagagatggattaccagtggaactaacactctctt tctctctccacccctcccccttggagaccacacagactctggccaaagcagactcgcgccca gctgcacctctcgggtctcggagtgttattctacacttgcctgggctcttctgggtggcg acgttcgctggaactgtgctgcgacacatctcctcgtgtgacacacttcaaccctgctcc ccaaacttggtaccatctatggcctcctcggatgtctcgtgtgacacacttcaaccctgctcc gcttggtgcatgagctgtctcggcgccgctggcagctaggctcgagagcttgccagcttggatc gctgacgagctgttctgcagccagcagcatctggaagctgacgacacatgacagcttggatc ctggtctcatcagcgccacatggaatacacyctccgaccccgcaagtgctgtccacgactga tcgctctacctggacactctcgtatcatlc/lctctggccccgcgtcttcttggctgggg agagactactctgagggcagcgaggtgacaggttaagcgcgagagcttctacgctgctct ccactgaggcctctactcgtgcctctgtgtggtgctctctgtactggaagatctacaag gctgcgaatctcgcgtgggctcaggaagacaaatagctctaccatataccgagctggtga ggTGCGTATCTACGAATCC
HTR6d5	HTR6	G	A	P	P	cds	GE1148	CCAGCGCTGT GCGACT	AGGCTCTGGT TCTCTCA	CAGCGCTGTGCGACTgcacatctccccagcctctctgatgctcctacatggctgggttaactgta acagacatgaaccccatcatcaccactcttcatcgggacttcaagcgagctcggcgcaag tctctgcatgtccacgctgtcccgaggcgcagcgacgctgcctgcctccgactcactgcac ctctcacagcgccccggccgctcttagctacacaggtgctgcgctgcctcactgcac actcagattcggaactcagcagagctcaggcgctctcggcgctcggctcagcgccagctg ctgctctcggcagggcaccacaggaacccccgctgcacacaggcgctgcgctcgaattt ctcaaatcgaccccgcgagccgagctgcggctlg/a catcacttggactccccagaaac tgacccggcttggggctggccaatgggagctggatTGACGAGAACCCAGACCTT
HTR6U1	HTR6	C	A	Q	K	cds	GE1148	CCAGCGCTGT GCGACT	AGGCTCTGGT TCTCTCA	CAGCGCTGTGCGACTgcacatctccccagcctctctgatgctcctacatggctgggttaactgta acagacatgaaccccatcatcaccactcttcatcgggacttcaagcgagctcggcgcaag tctctgcatgtccacgctgtcccgaggcgcagcgacgctgcctgcctccgactcactgcac ctctcacagcgccccggccgctcttagctacacaggtgctgcgctgcctcactgcac ccgactcagattcggaactcagcagcagctcaggcgctctcggcgctcggctcagcgccac gctgctctctcggcagggcaccacaggaacccccgctgcacacaggcgctgcgctcga atttctcaacatcgaccccgcgagccgagctgcggcgcaatcacttggactccccagaaac tgacccggcttggggctggccaatgggagctggatTGACGAGAACCCAGACCTT
HTR6U2	HTR6	G	T	A	A	cds	GE1316	GTCTCACGGA CGGTCCC	CTCCGAGCCT GACTGG	GTCTCACGAGCGTCCCGctcagcctgcgtctcgcggggccctctatctgctctccgcacc ctatacctctctgcgctccacctcggctctccttggctccagcgccggcgcccaacgaatag caccggcctggggcgagggcgccgctcggcccgccggggcgagcgctgggtggcgccgcgc tgctggtgcatcgcgtgacggcgctlg/lgccaaactcgtctgactcgcgctcactgcac tcagcccgctgcgcacacgttcaacttctcttgggtgcgtctcgaactgaactgatgg tggggctgggtga gcgcggcgccatgctgaacgctgtacggcgctgggtgctggcgcc ggctctgctgctctggacgctctcagctgattgctgcgagcgctctcactcactcgaactctg ccctacagcctggaccgctacctgctactctctgcgctgcgtacagctgcgactgacg ccctgcgtcccttgcctctgctctggcgctggagctcctgcgctcctgcctctctctgccc ctgctggtgggtggcagagctgggcagcagcgcccgctcctgcctcctgcctgctc ggcagagctgctcttctcttggctcggggctcactctctctcctgcctgcctgctccat gcttcaactactcaggaactcctagctgcccgcgaagcgccgtcaggtggctcctccac acccaatnctnctgacccgccc

FIG. 5FFFF

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
HTR6u3	HTR6	C	A	P	T	cds	GE1148	CCAGGCCGTGTGCGACT	AGGGTCTGGGT TCTGCTCA	CCAGGCCGTGTGCGACTGcaatctccagagcctcttcgagtcctccacatggctgggttactgtga acagacacatgaaccccatcatctaccacattctatcggggacttcaagcgggcgctggggcgag ttcttcgcatgtccacgctgtcccgccgagccagccagcctggctcctcactcgcatctcactgcac ctctcacaggcccccgcgccttagctactacagcaggtgtgtg[c/a]cgctgccccctgcg ccgactcagattcgagctcagacgagctcagggcctctcgggctcgggctcaggtcagcgcca gctgctgtctctgagcgagccacacagaccccgctgccccacagggcgctgctgcgcgtca atttctcaactgagaccccgagcccgagctcgccgcctacacttggcactccccacgaaac tgacccgggcttggggctggcccaatggggagctgggattgagcagAACCCAGACCT
HTR6u4	HTR6	C	T	A	A	cds	GE1148	CCAGGCCGTGTGCGACT	AGGGTCTGGGT TCTGCTCA	CCAGGCCGTGTGCGACTGcaatctccagagcctcttcgagtcctccacatgggttactgtga acagacacatgaaccccatcatctaccacattctatcggggacttcaagcgggcgctggggcgag ttcttcgcatgtccacgctgtcccgccgagccagccagcctggctcctcactcgcatctcactgcac ctctcacaggcccccgcgccttagctactacagcaggtgtgtcctcgcatctcactgcac actcagattcgagctcagacgagctcagcgctctctcgggctcgggctcagcgccagctg ctcttctcgagggccaccccgagaccccgctgccacacagggcgctgcgc[c/t]gtga atttctcaactgagaccccgagccagctcgccgcctacacttggcactccccacgaaac tgacccgggcttggggctggcccaatggggagctgggattgagcagAACCCAGACCT
HTR7d1	HTR7	T	C	L	P	cds	GE1178	TTGCTTGGTGTGACAGTTATG	AGTATTAATG ACCTTACAGCA	TTGCTTGGTGTGACAGTTATGatcacggtgtctatctgttcttccatcttccactcactaggctac cttgggactcacagggccctctcacactctgtaggcagatagggaaatgcagcgagatgat tctctcgtctggcttctctcgcctccatcaccttaacctcaacttttggattgggtccaggaatg taaatgatgataaaggtgtcttgacgcgcaggaatttgggtatacgaatttactctaccgcagtg gcatcttataccccacatgctgtcatgttctatgactaccagatttaccaggttgcagagaa gaggtgtcccaacaaagttctctggcttctctcggttggagtgagcagcagctcatctgccttga atggcatgtgaagctccagaaaggttggaaaggtgtgcaaaccttgcgaactctctcaagcat gaaggaataaacatctccatcttgaagcgaacgaagaaagacccacccctggggtcatcgt cggggctttaccgtgtgctgctgcatcttctctctctgcagcagcagcccttcatctgtg gaccttctgcagctgcatacccatgtgggtggagaggaatcttctgtgctaggctatgcacac tctctcttaaacctttatatagtcttcttcaacggagacctgagggaccactctgcagctc ctccagtgagctaccggaatacaacgggaagctctcagctgcaggtcatcgaagacccga agc[c/t/c]tgctgagggccagagagaccttgagtttgcgtgTAAGTGCATTATTCATCT
IGF1d3	IGF1	A	G	-	-	noncoding	GE1192	GCGTTAATAAA ATAGCATTAGG	GATGCCATTGC ATMAATCAGA	GCGTTAATAAATAGCATTAGTctactgagccacacaccttcaactttttatcaactcaaa gtagtgctactgtccacaaattggaatttgggggtgcaggcagaggtgtggaattttttaa gtlagaaggctccattgtttgttggctctcaacttagcaaatatagcaataatatcca[a/ g]tctctgaaacttgatcaagagataggaataaagcggggaaagaaatcttatagggcaata gaagaatttaaaagataagtagtcttctattgtatttgcctctgtcttaaacagatatt cagcaggtggggaataatgaagaacagaaataatgatttgcctctgtcttaaacagatatt tgcgaattccccctggggatccttggcaatttactgtttatagaacatctctctctc ccagacattcaaaagagcagtagctctcatgaagaacatcactgcatcttgggaattgtg gaagattctcttatgaatgggggttattctactgataaagaagaatttatgagaattgtgtg aaagatggcttaacaaattgtgaagatttttcttcttctgttttctttttttttttttta ctttacagcttcttatgaatttcttaattgtcmaaatgcttgggtttctttctttttttta tctcagaattgaggaaataaagttaaacccacatagactctttaaactataggctagataga tgtattgtgactgttgaagctataatcagactatttaaaattgtttgtctattttaacttaa taagattgtgctaaatttatlagagcagacctgttggctctctccagagaagaagatttccat tcaattcacatgcttctccacaatatttcaagaataaatttgcatttgcatttgcatttccat

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
IGF1d3 ₆	IGF1	C	T	C	C	cds	GE591	GAAAGCAGATT GCACCTTAC	CCACCCAGGTG GGCTTA	GAAAGCAGATTGACCTTAAATgagggcagcctctctgtgatttggtagagacaagccacaggggta 253 tggctccagcagtcggaggggcctccagacagcagcctctctgagtgagtgcttggctccggagc tgtagatcaaggaggctggagatgattgacacccctcagcctgccaagctcagctcgctctgt csgtgcctcagcgcacacagacatgccaagaccagaggtTAAGCCACCTGGGTGG
IGF1d3 ₇	IGF1	C	T	-	-	noncoding	GE578	AGGCCGCTTGA GTTGCT	GCTGGATATT CATTTGTTCTAA T	AGGCCGCTTAGTTCGTgagatgcaaggaaattctataaaacccattcatagcatagctagaga 807 ttggtagattgaaatgctctcagcatctcagttctctgtcagtgaaagctatccaaataaactctggccaa ctagttgtataaagctcaagctcaactctcttaaacactcttcaaaatattgaggaagcatttg attttcaatttgaatttgaattctgatttggatttcttgaatcaaaagataagtgaaagagagga aaggaagaaagaaagagaaacaaagagattctaccagtgaaagggaaattcaattactcttt gttag/c/tjactcactgactctctcagctactacatactgtaaaaccttggtaaacac tataataattctctattcttgaaaacacaaatgattcccttctctaggccaataaagga aagtgatccaaattgaaataatcaaaataatataataaaagtcacaagttatctctctta acaaacttactcttcttagctgtatatacttttttaaaagtttcttaaaatagctgtg actagagtttctcagttgaaagggcaaaactccatcacaaagaaatttcccatgctctcaga aggttagcccttagctctctgtgaatgtgtttatccattcaactgaaatttggatcaagaaag tccactggtagttagtactatcattatagcctatagcctagaaatgacccctctcgcagatcaagatt tctcatttagaacatgaaatttattccagc
IGF1u1	IGF1	C	A	A	D	cds	GE638	GGAACCACTTG TTCTCAATGC	TTTCCGTTTTTC TCCATGTTTT	GGAACCACTTGTTCTCAATGCaattattttgtgatgtttacagtatcagcccccattctaccac 419 aagaaacagaaagctctcagagaagaaaggctggccaaagacacatccaggagggaacagagga ggggacagaaagcaagctctgcagatcagaggaagaaagagagagagagagagagattggaagta gaaatg/c/a/jtgaatgcagagccaaagaaagaaatgaaggacagagagattaaacagacagag gcaagtagatgagagagagcagacagcaagaaatgaaagcagaaatacaaatagaggaatga agaaagtaggcctcgtcgtgagctagatgatgatgtaggaatagaaatgaagtaaccttttagagaat ctcgttaagAAACATCGAGAAACGGAA
IGF1u1 ₀	IGF1	A	G	-	-	noncoding	GE588	TCATAGCCTAG AAATGATCCC TAT	AGGGTTTGCTAT CAATTGTTTT	TCATAGCCTAGAAATGATGCTTATctgcagatcaagatttctctattagaaatgaattatccc 847 agcatctcagatcttctcagctcaccttagaacttttgggttaaaagtaaccaggtcttgaattatctc atgcaaatctctatatttcaattttggaaagctctatatgaaacaaacaaataacactcttcagttt ttctccctcctgggtcctccagagcagagggccagaaacaaacaaacaaacaaacaaacaaacaaac tgaatatatgcaaaagagggccctcttagtggccagcaatctctgctcagtcacacagatctc ttaaactctcagctccacatatttgaattgagcctcagcagatgcttagcaatttctaatcac tttgagcagatgaaagaaacataacatttttgcctctgctcttcttccagacatacagag ttctgtggaataagatctggaactctctcccaagatggcacttcttttatttcttctccca gtgtgaccttttaaaattatccctcacaacaaactttatagcgactctcttgcagacttaac la/g/jtgtttctgcatagtttagatgataattctaaagtgctctagctattctctcac ttaaactctccagctcaaaatcccccagaggaagctgaaagtgcaactgccaatatta tcttttaacttttccacacataatctctcactgattataaataaattgaaataaact catataaccaattcactatttttttttaagaaatataaactagaAAACAAATTTGATGCAACCC CT

FIG. 5HHHHH

Poly Id	Gene	ref N°	alt N°	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
IGF1 ₁	IGF1	T	G	-	-	noncoding	GE602	CCACACATAA TCCCTCCAC	CACATTGGCAT AGCTGGC	CCACACATAAATCTCCCAACTGGattataataataatgaaataaactcattatataccaattcac tatttatttttaagaattaaactagaataaacaanaattgatgaaacctgggaagtcagttgat [t/g]actatactacagcagagatgactcagatttctgtatagaaggagcaacaaatggtccaca ccaaacttcaagcttctgtccgaattgtctttataaattctggaatgaggccaattcca agataattgaaaagacagataaacattggtaagaatgagctttcaactcagactatttcca atttaattgaccatactggtactttagtcaaaattctgtctctcttcccacaaataatttcaa gtattattgaaacttttaagatgagcagctccctgaaanaagttaagcagctctccaccaga atccactctctagggatgaaaatctcttaacccccctcctacacacagacacacacac ac tcaacttctggaaaattttattaaaaacaaacaaacaaacaaagccttccacccttggaaa tcccttccctctctggaaactgaattgtgtgtagatgaacacatctcgtctctgggtccag ggttctgtactattttagtgcacttgggaaggcttgaataaagaatgtagacattttgct ttcccaatttattgttggccacgctATGCCAATCG
IGF1 ₂	IGF1	T	C	-	-	noncoding	GE603	TTTTATATAC TGAGGCTTAA AGT	AGATATACCAT TTTATATAGC ACTCT	TTTTATATACTAGGCGCTTAAAGTAaactactacttattttttggcccaaaatgcactgatgt aaagtggaaaataataaaacagagcttcaaaactcttcaagcccccacttgaccactccaa aactcatagaaagtcaactctgtttaaactcccttaactgattttgtttggatatttatctttgac ccgtgctaaacacacactgcaggaggactctgaaaccccaagctgtctacttacaattttatct gtgtctgtatcatcatgaaatgtctattcaaaataatcaaaacttcaaatcagcagacttat attcagtttacaataaaggccctac tgaagaatgggattcacatcatgatttctgctcatgttttggtaanaagatttaagaacta t/c]gataataaactacagacactgaataatttccctgctcttggaaacacagaaaataat gactggcaattctgtacatctgtctgttggaaagacataatttttcaataataatttcgattg tatttggaaattatttcaaatccactatggcagaggaatacaacttcaatcagacttcaaaaat gtaactaaattgaatcattatcttactgttctaataagcattttgaaaatgattatggcta GAGTGTCAATATAAATGGCTATACT
IGF1 ₃	IGF1	G	A	G	E	cds	GE642	AAAAATGCTTC TGCTCTTAOT	GAATGCCCAA TGACTTCAA	AAAAATGCTTCTGTGCTTAGTttttaaattgcaaaagtcatttattttgtccacatgcccaaa aaagtcttactcaataaacttctgcagaagaaggagagagagagagagagagagagagagag gttctctgtctaacagtgctgtgttttgtagataaatgtaggattctctctcaaatccctctct gtttgctaaattctcagctgcactgtaattctcagagcagantgagccctgcagaatgaataaag tcccaaaattgaaaatgacatgtcttcaacatctccactctctctgtgatttttttctgtctc attatctctgtaaccaattattttcagacttgcacttcagaagcaatg/g]ajaaaaatca cgagtcttccaaacccaattattaaagtgcgttttgtgattcttcttgaagggttaaatattctac tctTTGAAAGTCATTGGGAAATTC

FIG. 511111

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
IGF1 ₄	IGF1	T	G	-	-	noncoding	GE688	TCATAGCCTAG AAATGATGCC TAT	AGGTTTGCA CAATTTGTTT	TCATAGCCTAGAAATGATCCCTATCTGcagatcaagattttctctcattagaaacaatgaattatcc agcattcagatcttcttcagtcacctttagaacttttttggtttaaaagaccaggtctgatatttc atgcaaa[ct/g]tctatatcttaccattcttggaaagctctatagaaaaacaataaacaatcttc agtttttcccactgggtccactccaggatcagaggcaggaaaaaaaagaatccctctgga tctctgaaatcatgcaaaaagaagccccaatttagtgagccagcaactctcttcagctcaacaag tatttactctcagtcacaacttatttgaattgagccctcaagcatctctgctcagctagctctaa tcaactatggacagatgaagaagaactatacatattttgcctctgcctctcttccagaacata caggtctctggaaataagatactggactcctctcccaagatggcactctcttttattctctgctc cccaagtgactctttaaaattatctccctctcaaaaactttataggcagctctctctgcagact taaacgtttctctgcatagttgataatcttaagagtgctatgacttattctctccac tcaattctatccagctcaaaaatcccccaaggaggagctgaagatgcactggccaatatta ctttcttaactttttcccaacataactctctccaactggattataaataaataaataaact cattatccaattctactatttttttttaatgaattaaacttagaAAAACAATTTGATGCAAAACC CT
IGF1 ₅	IGF1	T	G	-	-	noncoding	GE688	TCATAGCCTAG AAATGATGCC TAT	AGGTTTGCA CAATTTGTTT	TCATAGCCTAGAAATGATCCCTATCTGcagatcaagattttctctcattagaaacaatgaattatcc agcattcagatcttcttcagtcacctttagaacttttttggtttaaaagaccaggtctgatatttc atgcaaa[ct/tat]ctattctcttggaaagctctatagaaaaacaataaacaatcttcagtt ttctcccactgggtccactcaagatcagagccaggaaaaaaaagaactccctctgagctc tgaataatgcaaaaagaagccccaatttagtgagccagcaactctctctcagctcaacaagatt tcaactctcagctccaactatttggaaatggacactcaagcalt/gtcttagcaaatgtcttaa tcaactatggacagatgaagaagaactatacatattttgcctctgcctctcttccagaacata caggtctctggaaataagatactggactcctctcccaagatggcactcttttattctctgctc ccagtggtgacttttaaaattatctctctcaaaaactttataggcagctctctctgcagact taacaattttctctgcatagttgataatcttaagatgagtgctctatgacttattctctcac ttaatctctccagctcaaaaatcccccaaggaggagctgaagatgcactggccaatatta ctttcttaactttttcccaacataactctctccaactggattataaataaataaataaact cattatccaattctactatttttttaatgaattaaacttagaAAAACAATTTGATGCAAAACC CT
IGF1 ₆	IGF1	T	C	-	-	noncoding	GE688	TCATAGCCTAG AAATGATGCC TAT	AGGTTTGCA CAATTTGTTT	TCATAGCCTAGAAATGATCCCTATCTGcagatcaagattttctctcattagaaacaatgaattatcc agcattcagatcttcttcagtcacctttagaacttttttggtttaaaagaccaggtctgatatttc atgcaaa[ct/tat]ctattctcttggaaagctctatagaaaaacaataaacaatcttcagtt ttctcccactgggtccactcccaagatcagagccaggaaaaaaaagaactccctctgagctc tgaataatgcaaaaagaagccccaatttagtgagccagcaactctctctcagctcaacaagatt tcaactctcagctccaactatttggaaatggacactcaagcalt/gtcttagcaaatgtcttaa taggaacagatgaagaagaactatacatattttgcctctgcctgttttccagaacatacagg ttcttggaataagatactggactcctctcccaagatggcactctttttattcttttctccca gt/c]gtgacttttaaaattatctctctcaaaaactttataggcagctctctctgcagact taacatgtttctctgcatagttgataatcttaagatgagtgctatgacttattctctcac ttaatctctccagctcaaaaatcccccaaggaggagctgaagatgcactggccaatatta ctttcttaactttttcccaacataactctctccaactggattataaataaataaataaact cattatccaattctactatttttttaatgaattaaacttagaAAAACAATTTGATGCAAAACC CT

FIG. 5JJJJ

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence	
IGF1u1 7	IGF1	A	T	-	-	noncoding	GE1192	GGCTTAATTAAG ATAGCATTAGG T	GATGCCATTGC ATTAATCAGA	GGCTTAATTAAGTACATTAGCTTCTATCTAGCCACCCACCCCTTCAACTTTTATCACTCAAA gtagtgactctccaccacattggaatttggggtgaggggagggaggtggaatttttttataatc gttagaggctccattgttttgggtctcacaacttagcaaatgagcaatataatattatccaatc ttctgaacttgatcagagcatggaataaaccggaagaaagatcttagcaaatatggaag aatttaagaataagtaagttcccttattgttttggcactctgctctaaagagatattcagc aagtgagaaaaataagaacaaagaaaaatacatagattaccctgcaaaaatagcttctgccc aaatcccccttgggaatcccttggcaatttactggtttatagaagacatttccctccaccag acatctcaagagcagtagctctcatgaagaacatcactgctcatttgggaatggttggaaag gtattctcttatgagatggggtattctactataaagaagattttatgagaatggttgaag agatggctaaacaatctggaagatttltgtttcttgggttttttttttttttttttttt la/tltagagttttagaatttcttaattgttcaaatgacttgggttcttcttctttttt talcagaatgggaataataagtttaaacccacatagactcttttaaaactataggcttagaaa tgatgttggacttgggaagctataacagactattaaaatggttttctatttttaadcttaa aagattgtctaatatttagagcagaacctgttggctctctcagaagaagaatcttcccat tcaaatcacatggtcttccaccaatatttcaaaagataaattCTGATTTATGCAATGGCATC	972
IGF1u1 8	IGF1	G	A	-	-	noncoding	GE683	TTTATATTAC TGAGGCTTAA AGT	AGATATACCAT TTTATTATGAC ACTCT	TTTATATTACTAGAGCCCTAAAGTAAactactactatttatttggcccaaaatgcactgagt aaagttagaataaatataaacagagctctaaatctcttcaagccaccatgaccctcacc aaacttagcaaaagtcactctgttaactcctgaacctcaal/gajctgtcacttactctt ccgtctcaaacacactcagagagactctgaacctcaal/gajctgtcacttactctt atctgtctgtgtatcatgaataatgctctatcaaaatatacaaaccttcaaatatacagcagc ttatatcagtttacaataaaggcccaatcaccatgcagatcttcttggtaaaaggttaatga actatggaattgggattacatcatgtatttggctctcatgtattttatcacactataggcaa gtgtgataataaaactacagacactgaattaaattccccctgactttgaaccagaaaaaat gaatggcattcgttactctgtcttagtgaagaagcatatttttataaatttaattctgttg tattgaaattatattcaattcacttattggaaggaataatcaatccttaagaacttctaaaat gtaactaatgaatcattatcttactgttcttataagcatatttgaagaatgtatggctc GAGTGTGATATAAATGGTATATCT	741
IGF1u1 9	IGF1	C	G	-	-	noncoding	GE1191	TTTATAGGAAG TACATTGGAAG AAC	ACAACTACAA AATAGCACCAT	TTTATAGGAAGTACATTTCAGACMACgaagt agagggagtgaggaaacagaactacagagat aggaagaccctcttggaggtgagagtgagatgcacgcagcagagatcttctgtctgcaggtt acctgttaactttggagacacactaccacaaataaagtgttgataacatttaaaagatggcgttc cccaatgaataacacagaagtaaacacttccaaatgttcttagaggtgatttgcaccttgcacaa atggctcctggagttggtagattgctgtgtgacttttcaataaagtctctatagaagaagaaaa aaatataatataatataatctttagtccctcctcacaaguccacaaatgcatgggtgtot aatatccagctgcactaaattlc/gjctcttgaatcttggctgctggagccatttattcagca acctgttaagtggtttatgaatttcttcttatttggcatttcttctacacactcctgggtgt ttgtttacagltgctgataaattctgttactataccacacacctctcttcaacttataat ttggcgaatttggcctctcacaagcagcagcaagtcgtcagaagcacaaccaattctaacccac aagatccatctggcatttgaacaaataaagtgtgagatcattttatttaacacacaaagct tatttttccacatgcttcaaaaagaataatgcaacttcaactcaaaagagcttctcaaatgata tttttaggcatagttttaacataagaagtttcttcaactcaaaagagcttctcaaatgata gttaatgtaacacctaatttagtaacttctcttcttatttttccatagagacactatgataa tttagcatatcaattatcacagatatatacaacagatgataaaactctgttttttagtataATGG TGCTATTTTGTAGTTTGT	993

FIG. 5K KKKK

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
IGF1u2	IGF1	G	A	-	-	noncoding	GE678	AGGCGCTTGA GTTGCT	CCTGGATAATT CATTTGTTCTAA T	AGGCGCTTCAGTTGTCGagatcaaggaaattctataaataaccatcatagcatagctagaga ttgggaattgaatgctctctgaatctcagttcttctgcagtgagagctcaaaatcaactgagccaa ctagttgttaaaa[g/a]ctaaacagctcaatctctcttaaacaccttcaaaatataatgtgggaaga ttgtatttcaattgatttgaattctgatttgggtttttatgaatacaaaagtaagtgaaaga gagaaaggaaacaaaggagaaacaaagagatttccacagtgaaaggagaaatataattact ctttgttagcactcaactctctctagctgactacacatctcagtagcaaaccttgttcaaac tataaaataattctcatctatttgaaacacacaaatctctctttcttaggcaataaagga aagtgaicccaaatttgaaatttaaaataataataataaaaaagtcacaaagtctactctttta acaaactttactcttactctcagctgataatacttttttaaaagtttctgtaaaatagtctg actagagtttcagttgaaaggcaaaaacttccatacaacaaagaaattcccaacgtctctcaga agggtagccctcagctctctgtgaattgttttctcattcaacagaaattgtgtatcagaagag tccactggttagtgtactagctcatcatagctcagaaaatgatccctactctgcagatcaagattt tctcattTAGAACAAATGCAATTATTCAGC
IGF1u2	IGF1	T	G	-	-	noncoding	GE678	AGGCGCTTGA GTTGCT	CCTGGATAATT CATTTGTTCTAA T	AGGCGCTTCAGTTGTCGagatcaaggaaattctataaataaccatctcatagcatagctagaga ttgggaattgaatgctctctgaatctcagttcttctgcagtgagagctcaaaatcaactgagccaa ctagttgttaaaa[g/a]ctaaacagctcaatctctcttaaacaccttcaaaatataatgtgggaaga ttgtatttcaattgatttgaattctgatttgggtttttatgaatacaaaagtaagtgaaaga gagaaaggaaacaaaggagaaacaaagagatttccacagtgaaaggagaaatataattact ctttgttagcactcaactctctctagctgactacacatctcagtagcaaaccttgttcaaac tataaaataattctcatctatttgaaacacacaaatctctctttcttaggcaataaagga aagtgaicccaaatttgaaatttaaaataataataataaaaaagtcacaaagtctactctttta acaaactttactcttactctcagctgataatacttttttaaaagtttctgtaaaatagtctg actagagtttcagttgaaaggcaaaaacttccatacaacaaagaaattcccaacgtctctcaga agggtagccctcagctctctgtgaattgttttctcattcaacagaaattgtgtatcagaagag tccactggttagtgtactagctcatcatagctcagaaaatgatccctactctgcagatcaagattt tctcattTAGAACAAATGCAATTATTCAGC
IGF1u2	IGF1	T	C	-	-	noncoding	GE676	AGATAGACAG AGGCCCAGG	TTGGCCAAAT AAAAATGATGA TGT	AGATAGACAGAGCCCGAGggattttggaagctgtcttattctctgcccacatccccaccagcc cttatatttttagtactctgcctcagaattttgagagctgtgcccagctgaactcttgaagatta aagaaacctcactgaaacaataatttccagttgttccctctctttttctctctttgtggagata gggtctgcactgtccccagctggagtcagtggtgatctctgcgtcactgacacacccacc tctctgggtt[c/e]aagcgattctctgcctcagctctcgtgagtcagtggtggttacagaccacca tccactatccggctcaattttttggatttttaataagagacggggttttaccactgtggccaggtt ggactcaaacctctgcactgtgatttgcctccctcagctcccaaaattgctgggattacaggca tgagcacacacacccctgccatgtgttccctcttaattgatactagcttccatcaaaatgat ctctctctcatcttctcaactatcttgaagggtcttccaggggcaaaaaaatccaaagcttt tttaagttcaaaaaaagagagagagacacaaacaaattgttactgtctcaactgaaatagag ttaagatggagacagaggtttctcctaataacgggagctgaaattacctttcaacttcaaaaacatg accttcccaaatccttagaattcgtctttttttatattactgagcctaaaagttaaaCATTTACTC ATTTTATTTTTOCCAA

FIG. 5L1111

[illegible]

FIG. 5MMMM

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
IGF1u2 5	IGF1	T	C	-	-	noncoding	GE1192	GGCTTAATAAA ATAGCATTTAGG T	GATGCCATTGCG ATMAATCAGA	GGCTTAATAAAAGCATTTAGCTctctctagccaccaccaccccttccaactttttttatcactcacaa gtagtgactgtctccacaattgtgaatttgggggtgagggcgagagtgaggaattttttttaa gttagaaggctccactgtttgttggtctccaaacttgcgaataatgagcaataatataatcccaatc ttctgaacttgatacagagctagggataaaccgagggaataaagatctcttaggcaaatlagagag aatttaaagataaagtaagttcccttattgtttttgtgactctgtctcaaacagataattcagc aagtgtagaataaagacaagagaaaaatacatagatttaccctgcgaagaaaatacgtctctgcc aaantcccentggggaatccttggcaatttactggtttatagagaacatctctctccaccac acattccaaagagcagtagctctctgcgaagcaaccactgactctctatcttgggaaggttggaaa gattctctctatgagatgggggttatctactgataaagaagaattatagaaaatgttggaaaag agatggctcaacaactctggaagattttttgttctgtgtttgttttttttttttttttttttt atacagctcttatgaattcttcaatgttccaaatgacttgggttttttttttttttttttttt eqaattgggaataaagtttaaccacacataagactcttaaaactatg/cjagggctagatagaaa totatgttgacttgttgaagctaaatcagactatttaaaagtgttttctctatttttaacttaa agaattgtgctaaattatagagcgagaacctgttggctctctcagagagaagaactcttccat tcaaatcacatggctctcccaaatattttaaagaagataaaattgattttatgcaatggcattc ctattatttttagtatactctccacagaatttttagaggggtgaccgaagctgaacctccagaatta aaggaacctcactgaaacacataataatccagctgttccctctctttttttttttttttgtgagatg gggtctcgactgccccccagcgtaggtgcagtgagctgatctcggctcactgcacacctccacc tcttggtttaagcgaattctctctcagctctcgttagtgagtgaggtacagacagccacacac tatcgcggtcaatttttttggaattttaaagagacggggtttaccatgttggcagagcttgagc tcaaaactcctgacctgtgatttggccgctcagctcccaaatgctgggtatcacagcagatgag ccacacacacctggccatgtgttctcttcaatgtatg/alattacaaggatcttcaacatgat ctctctctctctcttctcaactatcttgatgggtgtcttcaaggggaaaaaaatccagcttt tttaagtaaaaaaagagagagagacacaaacaaatgtactgctcaactgaaatlatgag ttaagatggagacagaggttctcttaataccgggagctgaattaccttctcaacttcaaaaacatg accttccacatctctagaatctgctcttttttttatattactgagggctaaaaagtaaacATTACTC ATTTTATTTTGGCCCA
IGF1u2 6	IGF1	G	A	-	-	noncoding	GE676	AGATAAGACAG AGGCCCAGG	TTGGCCAAAT AAATGAGTAA TGT	GAATAAGACGCCAGGagatttttgaagctgtcttttctgcccctccccaccacagcc ctattatttttagtatactctccacagaatttttagaggggtgaccgaagctgaacctccagaatta aaggaacctcactgaaacacataataatccagctgttccctctctttttttttttttttgtgagatg gggtctcgactgccccccagcgtaggtgcagtgagctgatctcggctcactgcacacctccacc tcttggtttaagcgaattctctctcagctctcgttagtgagtgaggtacagacagccacacac tatcgcggtcaatttttttggaattttaaagagacggggtttaccatgttggcagagcttgagc tcaaaactcctgacctgtgatttggccgctcagctcccaaatgctgggtatcacagcagatgag ccacacacacctggccatgtgttctcttcaatgtatg/alattacaaggatcttcaacatgat ctctctctctctcttctcaactatcttgatgggtgtcttcaaggggaaaaaaatccagcttt tttaagtaaaaaaagagagagagacacaaacaaatgtactgctcaactgaaatlatgag ttaagatggagacagaggttctcttaataccgggagctgaattaccttctcaacttcaaaaacatg accttccacatctctagaatctgctcttttttttatattactgagggctaaaaagtaaacATTACTC ATTTTATTTTGGCCCA
IGF1u2 7	IGF1	T	G	-	-	noncoding	GE682	CCACACATAA TCCTCTCCAC T	CACATTGGCAT AGCTGCG	CCACACATAAATCTCTCCAACTggattataaataaattgaaataactctattatcaccaattcac tattttatttttaatgaattaaaactagaaaacaaatttgtcgaacctctgggaagtcagttgat tactataactacagcagagaagtagcttcatctatagaaggagacacaaatgtcacaaacaa taacttcaagcttctgtctcagaaatttagatttttataattcttgaagggaacatttcaagat atttgaagaagaacagataaacattggttaagaatgagcttccaactcaggtctatttccaattt aattgacataactggaacttaggtcaaatctgtctctctctctcccaaaataataataaagtat tal/gjtggaacttttaagatggcgagttcccttgaaaagtttaalgcagctctccatcaga atccactctctagggaatagaaattcttcaacaccccaacctacatacacagacacacacac acacacacacacacacacacacacatctcaccctgaagtcctatcgaatactgaagaagaa tcaactcttgaaaattttataaaacaaacaaacaaacaaacagctctccacctctggaaa tccctctctctctggacgtcaagtgttgttagatgaataacacatctcatgctctggctccag ggtttctgttactatatttctgactctgggagagaggttagaataaagagctgagcacatttgc ttccacttctatorttggccacgttattgcaattg

FIG. 5NNNNN

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
IGFlu2 8	IGF1	T	G	-	-	noncoding	GE1192	GCCTTAATATA ATAGCATTAGG T	GATGCCATTGC ATNAATCAGA	GCCTTAATATAATAGCATTAGGTCATCTATAGCCACCACCACCTTCAACTTTTATCACTCACAA GTTAGAGGCTCCACCAATGTGAATTTGGGGTGCAGGGGAGGAGTTGGAATTTTAA GTTAGAGGCTCCATTTTGTGTGGCTCTCAAACTAGCAAAATAGCAATATAT [T/G]ATCC AATCTTGAACTTGACAGGACATAGGAGTAACGCGGGAAGAAATCTTATAGGCAATA GAGAAATTAAGATAAGTAAGTTCCTTATGATTTGTGCACTGTCTCAAAACAGATAT CAGCAAGTGGAGAAATAAGAACAGAGAGAAATACATAGATTTACCTGCAAAATAGCTTC TGCCAAATCCCTCCTGGGAATCTTGGCAATTTACTGGTTTATAGAAACATCTCCCTTCAC CCAGACATCTCAAGAGCAGTAGCTCTCATGAAGCAATCACTGATCTATTGGGAAATGTG GAAAGTATCTCTATAGAGTGGGGTTATCTACTGTAAAGAAATTAAGAGAAATGTG AAGAGATGGCTCAACAACTGTGAAGATTTTGTCTGGTLLGTTTTTTTTTTTTTTT CTTACAGCTCTTATGAATTTCTAATGTTCAAAATGACTTGTCTTCTCTTTTTTTT TATCAGATGGAGAAATAAGTAAACCCACATAGCTCTTAAACATAGCTAGATAGAA TGATGTTGACTTGTGAAGCTAATCAAGCTATTAAATGTTTGTCTATTTTCAATCTTAA AAGATGTCTAATTTATAGAGCAGAACCTGTTGGCTCTCTCTCAGAGAGAAATCTTCCAT TCAATCATATGGTCTTCCCACTATTTTCAAAAGTAAATCTGATTTATGCATGGCATC GCCTTAATATAATAGCATTAGGTCATCTATAGCCACCACCCTTCAACTTTTATCACTCACAA GTTAGAGGCTCCACCAATGTGAATTTGGGGTGCAGGGGAGGAGTTGGAATTTTAA GTTAGAGGCTCCATTTTGTGTGGCTCTCAAACTAGCAAAATAGCAATATATCTCACT CTCAGAACTGTACAGGACATAGGAGTAACGCGGGAAGAAATCTTATAGGCAATAAG AATTAAGATAAGTAACTTCTTATGATTTGTGCACTGTCTCAAAACAGATATCTCAG AAGTGGAGAAATAAGAACAGAGAGAAATACATAGATTTACCTGCAAAATAGCTCTGCC AAATCCCTCCTGGGAATCTTGGCAATTTACTGGTTTATAGAGACATCTCTCTCACCAG ACATCTCAAGAGCAGTAGCTCTCATGAAGCAATCACTGATCTATTGGGAAATGTGGA GTTCTCTATAGATGGGGTCTATCTACTGATAAGAGAAATTTATGAGAAATCTGGA AGATGGTCAACAACTGTGAAGATTTTGTCTTGGTTTGTGTTTCTTCTTCTTCTTCTT ATACAGCTCTTATGAATTTCTTAAAGTTCAAAATGACTTGTCTTCTTCTTCTTCTTCT AGATGGAGAAATAAGTCAAAACCATAGCTCTTAAACATAGCTAGCTAGATAGAAAT [G/ C]TATGTTGACTTGTGAAGCTAATCAAGCTATTAAATGTTTGTCTATTTTCAATCTTAA AAGATGTCTAATTTATAGAGCAGAACCTGTTGGCTCTCTCTCAGAGAGAAATCTTCCAT TCAATCATATGGTCTTCCCACTATTTTCAAAAGTAAATCTGATTTATGCATGGCATC GCCTTAATATAATAGCATTAGGTCATCTATAGCCACCACCCTTCAACTTTTATCACTCACAA TCAATTTAGGACATATGTTTAAACATAGAGATTTCTTCACTCAAGAGGTTCTCTCAATGA TGAGTTAAGTGCACCAATATAGTAACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT AAATTAGCATCAATATACAGGATATATCAACAGTATGAAACCTCTGTTTCTAGTATAG TGATGATTTTGTGTTTATATAGAGAGCTTGGCCAAACGTTAATACGTTGAGAGCAAAA CAATAGGGAGAGCTGGAGCAAGATGACACAGGGGAGGAGTACTGAAACACCACTCCATTG GGAAGAGGCAAGTCCCTCCAGTTATGCTCTCAAGAGGAGTCTCAGACAAAGTCCACTG ATGCAATGGAGTGGAGTCCAGAGGAGGAGTGGAGTGGAGAGGAGGAGGAGGAGGAGGAG TTGAGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT ACCAGTGTGACCTTGGCAGTCACTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT GGGGCAATATGCTCTCACTCACTCAAGGGGTGTTAAGGTTTAAAGATAAGATCTAG ATTTTCTACCTGGGTGCTATAGGAGTCAACATCAGGCGCTGAGTTGTGAGATGCAAGG AATCTCAATAAACCATTCTATAGATAGTATAGATTTGGTGAATTTGATGCTCTGACTCTC AGTCTGTGAGTGAAGCTATCAAAATCACTGAGGAGTGTGTTTAAAGCTAAGAGTCACTC TCTTAAACATCTTCAAAATATGTTGGAGCTATTGATTTCAATTTGATTTGATTTCTGCT TTGGTTTATGATACAAAGATAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
IGFlu2 9	IGF1	G	C	-	-	noncoding	GE1192	GCCTTAATATA ATAGCATTAGG T	GATGCCATTGC ATNAATCAGA	GCCTTAATATAATAGCATTAGGTCATCTATAGCCACCACCCTTCAACTTTTATCACTCACAA GTTAGAGGCTCCACCAATGTGAATTTGGGGTGCAGGGGAGGAGTTGGAATTTTAA GTTAGAGGCTCCATTTTGTGTGGCTCTCAAACTAGCAAAATAGCAATATATCTCACT CTCAGAACTGTACAGGACATAGGAGTAACGCGGGAAGAAATCTTATAGGCAATAAG AATTAAGATAAGTAACTTCTTATGATTTGTGCACTGTCTCAAAACAGATATCTCAG AAGTGGAGAAATAAGAACAGAGAGAAATACATAGATTTACCTGCAAAATAGCTCTGCC AAATCCCTCCTGGGAATCTTGGCAATTTACTGGTTTATAGAGACATCTCTCTCACCAG ACATCTCAAGAGCAGTAGCTCTCATGAAGCAATCACTGATCTATTGGGAAATGTGGA GTTCTCTATAGATGGGGTCTATCTACTGATAAGAGAAATTTATGAGAAATCTGGA AGATGGTCAACAACTGTGAAGATTTTGTCTTGGTTTGTGTTTCTTCTTCTTCTTCTT ATACAGCTCTTATGAATTTCTTAAAGTTCAAAATGACTTGTCTTCTTCTTCTTCTTCT AGATGGAGAAATAAGTCAAAACCATAGCTCTTAAACATAGCTAGCTAGATAGAAAT [G/ C]TATGTTGACTTGTGAAGCTAATCAAGCTATTAAATGTTTGTCTATTTTCAATCTTAA AAGATGTCTAATTTATAGAGCAGAACCTGTTGGCTCTCTCTCAGAGAGAAATCTTCCAT TCAATCATATGGTCTTCCCACTATTTTCAAAAGTAAATCTGATTTATGCATGGCATC GCCTTAATATAATAGCATTAGGTCATCTATAGCCACCACCCTTCAACTTTTATCACTCACAA TCAATTTAGGACATATGTTTAAACATAGAGATTTCTTCACTCAAGAGGTTCTCTCAATGA TGAGTTAAGTGCACCAATATAGTAACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT AAATTAGCATCAATATACAGGATATATCAACAGTATGAAACCTCTGTTTCTAGTATAG TGATGATTTTGTGTTTATATAGAGAGCTTGGCCAAACGTTAATACGTTGAGAGCAAAA CAATAGGGAGAGCTGGAGCAAGATGACACAGGGGAGGAGTACTGAAACACCACTCCATTG GGAAGAGGCAAGTCCCTCCAGTTATGCTCTCAAGAGGAGTCTCAGACAAAGTCCACTG ATGCAATGGAGTGGAGTCCAGAGGAGGAGTGGAGTGGAGAGGAGGAGGAGGAGGAGGAG TTGAGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT ACCAGTGTGACCTTGGCAGTCACTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT GGGGCAATATGCTCTCACTCACTCAAGGGGTGTTAAGGTTTAAAGATAAGATCTAG ATTTTCTACCTGGGTGCTATAGGAGTCAACATCAGGCGCTGAGTTGTGAGATGCAAGG AATCTCAATAAACCATTCTATAGATAGTATAGATTTGGTGAATTTGATGCTCTGACTCTC AGTCTGTGAGTGAAGCTATCAAAATCACTGAGGAGTGTGTTTAAAGCTAAGAGTCACTC TCTTAAACATCTTCAAAATATGTTGGAGCTATTGATTTCAATTTGATTTGATTTCTGCT TTGGTTTATGATACAAAGATAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
IGFlu3	IGF1	T	C	-	-	noncoding	GE1326	GCTTTATTTT CCACATCATGC	CCTAGAAAGA AGGAATCA/TG	GCTTTATTTTCCACATCATGCTTACAAAAGAAATAGTGAATTTGCAACTTTAGGAGCAAA TCAATTTAGGACATATGTTTAAACATAGAGATTTCTTCACTCAAGAGGTTCTCTCAATGA TGAGTTAAGTGCACCAATATAGTAACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT AAATTAGCATCAATATACAGGATATATCAACAGTATGAAACCTCTGTTTCTAGTATAG TGATGATTTTGTGTTTATATAGAGAGCTTGGCCAAACGTTAATACGTTGAGAGCAAAA CAATAGGGAGAGCTGGAGCAAGATGACACAGGGGAGGAGTACTGAAACACCACTCCATTG GGAAGAGGCAAGTCCCTCCAGTTATGCTCTCAAGAGGAGTCTCAGACAAAGTCCACTG ATGCAATGGAGTGGAGTCCAGAGGAGGAGTGGAGTGGAGAGGAGGAGGAGGAGGAGGAG TTGAGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT ACCAGTGTGACCTTGGCAGTCACTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT GGGGCAATATGCTCTCACTCACTCAAGGGGTGTTAAGGTTTAAAGATAAGATCTAG ATTTTCTACCTGGGTGCTATAGGAGTCAACATCAGGCGCTGAGTTGTGAGATGCAAGG AATCTCAATAAACCATTCTATAGATAGTATAGATTTGGTGAATTTGATGCTCTGACTCTC AGTCTGTGAGTGAAGCTATCAAAATCACTGAGGAGTGTGTTTAAAGCTAAGAGTCACTC TCTTAAACATCTTCAAAATATGTTGGAGCTATTGATTTCAATTTGATTTGATTTCTGCT TTGGTTTATGATACAAAGATAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

FIG. 500000

[illegible]

FIG. 5PPPPP

[illegible]

FIG. 5RRRRR

FIG. 5TTTT

FIG. 5VVVVV

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
LIPC2 2	LIPC	T	A	M	K	cds	GE353	AGCAGCCTTG AGAGACG	TCACCAAGTCC CTATCTTTTAA T	ACGACGCTTTGACAGACGAGGGCTTCAGATGAAGCAGATGCCAGGTCAAGCACCCTCCCAAT CTATATTGGAGGAGCCATTGGGAGAGAGCTCAAGGTGTGAAACAACAAGAGCTGCTGATGAG ATCAGGACAGCTTACAGAGTGCAGCTCTTGGAGAACCAATCAGGGCTGTCAGATTCGAATCAATC TGGTCGGTAGGAAATGCTGACATCGCTTTTCTCTCTCGATTCTCACTAGCTGCTCATGCTCATA AAAGATAGAGGAGCTGGTGA
LIPC2 3	LIPC	G	C	G	A	cds	GE253	CACACTGGACC GCAAAAGG	AGTGTGTGAGT TATTAGGCATG G	CACACTGGACCGCAAAAGGCTTTCTATCCAGGAGCTCTCTCTGCCCCCATCCCGCTGCTC TTCAGGAATCTGTTCACCTCTCTCGAAGCCATGTTCACCTAATGGGTACAGCTGGTGCACA CGTCAAGGATTTGCCG[g/c]CAGTTCATCGGTGGAGCACAAGATTGGGAGATCACAGGT AACCATGCTTAATACTCACACACT
LIPC2 4	LIPC	A	T	Q	L	cds	GE475	AACTGATTGTG TCTGATTTTCT	TGGCAACAAGT GGTGCTTA	AACTGATTGTGCTGATTTTCTTTGTGATTCAGGGGCAAGGAATGCTAGTAATAAAGCTA TCTCTTCTATCAGCTGGATGAGGATCGGAGCTGATCATGATCAAGTCAAGTGGGAAA ACAGTGAAGTGGGCAATGTCTGGGATACAGGCTCAGACCATCACTCATGGAGCAGGGCG CGCACTAGGCTCTGTTGAGAGCAGTCAAGAGGAGGAGAAACCCAGC[a/t]AAGGT GACTGCTGAATCTCTCTCTTAACTGCTCATTAAGCACCCACTTGTGCCA
LIPC3	LIPC	T	G	V	V	cds	GE253	CACACTGGACC GCAAAAGG	AGTGTGTGAGT TATTAGGCATG G	CACACTGGACCGCAAAAGGCTTTCTATCCAGGAGCTCTCTCTGCCCCCATCCCGCTGCTC TTCAGGAATCTGT[a/g]CACTCTCTCGAAGCCATGTTCACCTAATGGGTACAGCTGGTGC CACAGTGTCAAGATTGGCGGAGTTCATCGGTGGAGCACAAGATTGGGAGATCACAGGT AACCATGCTTAATACTCACACACT
LIPC4	LIPC	T	A	L	Q	cds	GE253	CACACTGGACC GCAAAAGG	AGTGTGTGAGT TATTAGGCATG G	CACACTGGACCGCAAAAGGCTTTCTATCCAGGAGCTCTCTCTGCCCCCATCCCGCTGCTC TTCAGGAATCTGTTCACCTCTCTCGAAGCCATGTTCACCTAATGGGTACAGCTGGTGC CACAGTGTCAAGATTGGCGGAGTTCATCGGTGGAGCACAAGATTGGGAGATCACAGGT AACCATGCTTAATACTCACACACT
LIPC5	LIPC	A	G	G	G	cds	GE323	CTCCCGGTAA CCCTTACC	CGGCCCATGAC TTTCATTCTC	CTCCCGGTAAACCTTTACCCCTGTCTTCCATTAGGCTGGATGCCGCGG[a/g]CCTTGT GAGGAGAGTCCCCCAGCAATCTCTTCCAGATGATGCCAATTTGTGGATGCCATCAAC CTTACCCGGAGCACATGGGCCCTGAGCTGGGATCAACAGCCCATAGGACATGACTCTCT ATCCCAACGCGGCTCTCTTCCAGCTGCTCTCTAGAGCTCTACAGACATATGCCAG CACGGCTTCAATGGTGGAGATGAAGTCAATGGCCG
LIPC6	LIPC	A	G	N	S	cds	GE323	CTCCCGGTAA CCCTTACC	CGGCCCATGAC TTTCATTCTC	CTCCCGGTAAACCTTTACCCCTGTCTTCCATTAGGCTGGATGCCGCGGACCTTGTGGAG GAGTGCCTCCAGCAATCTCTTCCAGATGATGCCAATTTGTGGATGCCATCAAC CTTACCCGGAGCACATGGGCCCTGAGCTGGGATCAACAGCCCATAGGACATGACTCTCT ATCCCAACGCGGCTCTCTTCCAGCTGCTCTCTAGAGCTCTACAGACATATGCCAG CACGGCTTCAATGGTGGAGATGAAGTCAATGGCCG
LIPC7	LIPC	T	G	N	K	cds	GE323	CTCCCGGTAA CCCTTACC	CGGCCCATGAC TTTCATTCTC	CTCCCGGTAAACCTTTACCCCTGTCTTCCATTAGGCTGGATGCCGCGGACCTTGTGGAG GAGTGCCTCCAGCAATCTCTTCCAGATGATGCCAATTTGTGGATGCCATCAAC CTTACCCGGAGCACATGGGCCCTGAGCTGGGATCAACAGCCCATAGGACATGACTCTCT ATCCCAACGCGGCTCTCTTCCAGCTGCTCTCTAGAGCTCTACAGACATATGCCAG CACGGCTTCAATGGTGGAGATGAAGTCAATGGCCG
LIPC8	LIPC	C	G	T	T	cds	GE323	CTCCCGGTAA CCCTTACC	CGGCCCATGAC TTTCATTCTC	CTCCCGGTAAACCTTTACCCCTGTCTTCCATTAGGCTGGATGCCGCGGACCTTGTGGAG GAGTGCCTCCAGCAATCTCTTCCAGATGATGCCAATTTGTGGATGCCATCAAC CTTACCCGGAGCACATGGGCCCTGAGCTGGGATCAACAGCCCATAGGACATGACTCTCT ATCCCAACGCGGCTCTCTTCCAGCTGCTCTCTAGAGCTCTACAGACATATGCCAG CACGGCTTCAATGGTGGAGATGAAGTCAATGGCCG

FIG. 5WWWWW

FIG. 5XXXXX

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
MPLu4	MPL	C	G	L	V	cds	GE482	CTCTGGTGCCA CAATCCCT	CCAGGATCCC CTGCGTA	CTCTGGTGCCACAAATGCTTgtgcacgaaggacttaagctgctccctgctgacataccctgtagt ggcctcccccccaacttgcactggaaggagatccaggtggat[c/g]tgcgaattggag tggcagcaccatgctctggcgcacgaagactgtatcaactccgatacacaggaagaag ccatcaggactggaaggtatggtcaagcaacaatgccacagactctactACGGAGGGAATCCC TGG
MPLu5	MPL	G	A	E	K	cds	GE491	AGAGCTGAGC CATAGACTGT	TGGGGCAAGAT TGAAGGTAG	AGAGCTGAGCATTAGACTGTgtactcagagtctctgagtgcgcctgctcttgccctcaggcctgc ggcctccccccagtatcatcaaggccctatgggtggagcagcaggagggaacttcagatcagctgg ggaggcaggcttcagaaatcagtgattctctggagtag[c/a]aaactccgatggatccacagctgg atcccaagaactccactggtccacggtatcacagctgattgcgcagaaaactgcctgcctctgt ctgcagaggctcactcagctctgtcttgaccagttctcattgtctgcagcccacaatgccctg gcaagatggaccaaaagcagacctcccccaagtcacagagatagtgtagctcttctgtgcccaactc tatactctACTCTCAATCTTCCGCCA
MPLu6	MPL	C	A	R	R	cds	GE490	GGGTGGAGGC TCTCTCAG	CAGCCTTCCTT AGAGATAATCTT TTTA	GGGTGGAGGCTCTCTACGtcgacgagcagacctagattgtgaagctgggattttctcccaagg cttcagctctgcacgacgaggtgggaagctgacctctcctcaggacctccagctgggaactctctac tgacctcagctgg[c/a]agcgaacctgatgggattctctctggctcctgggagatccttgg cctctctgtgactgtggacctgctctggagatgcagggtgagtcacaaagggaataggagatggg ggaggaTAAAGAGATATCTTAGGGAAGCCTG
MPLu7	MPL	T	C	F	S	cds	GE472	ACGTGGGGCTG TATCTGACA	CAGGGCTCCTT CTTCTTG	ACGTGGGGCTGTATCTGACAggaaccttcagggtctggcctggaggggattggggcccagcttcc tgaaggggagatggcttaaggcagacagctggcggagaagatgccctctctggccctctt/ c]atgggtcacccttcgctctctctggccctcaaaactgtggcccaagtcagcagccaaggtga ggtcacagagggctggagatcaactatgccccCAGGAGAGGGAGCCCTG
MPLu8	MPL	C	T	S	S	cds	GE472	ACGTGGGGCTG TATCTGACA	CAGGGCTCCTT CTTCTTG	ACGTGGGGCTGTATCTGACAggaaccttcagggtctggcctggaggggattggggcccagcttcc tgaaggggagatggcttaaggcagacagctggcggagaagatgccctctctggccctcttca tgatcaacctc[t/t]gtcctctctggccctcaaaactctcagctcagcagccaaggtga ggtcacagagggtggagatcaactatgccccCAGGAGAGGGAGCCCTG
MPLu9	MPL	G	A	G	G	cds	GE491	AGAGCTGAGC CATAGACTGT	TGGGGCAAGAT TGAAGGTAG	AGAGCTGAGCATTAGACTGTgtactcagagtctctgagtgcctctgctctggcctcagcctgc cggctccccccagtatcatcaaggccatgggtgg[c/a]agcagcagcggggaacttcagatcag ctggaggagccagctcccaaaaacagtgattctctggagtcagactcctatggccccagag atcccaagaactcactggtccacggtatcacagctgattgcgcagaaaactgcctgcctgt ctgcagaggctcactcagctctgtctggaccgtctctcattgtctcagcccacaatgccctg gcaagatggaccaaaagcagacctcccccaagtagagaagatgctgacctctcttctgcccaactc tatactctACTCTCAATCTTCCGCCA

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
NGFBd9	NGFB	G	A	A	A	cds	GE1185	CACATCCATAC TGCCTGAGT	AGGCGCCGAGG AGAGTG	CACATCCATACCTGCTGAGTGTGAGCCCGGGTACGCGCTGTTGCTCCGGTATAACCATTTGCTAGCA CACCTTCCCTCTCAGAGTGCCTGTTGAATGAACCTCTCTGATCCCTCTGGAGTCA ACTTGAAGGCCGAGAACTGCTTTTGAAGTCAATTAGTCACTCAAGTCAAGTCAACCTCATTCT TTTTCTCCAGTGCATAGCTAAATGCTCATGTTGTTTCACTCTGATCAGTCTTTCTGA TCGGCATACAGGCTG/ALGACACACTCAGAGGCAATGCTCTCAGGACACCATCTCCCA AGTCCACTGACTAACTTCAGTCTCCCTGACACTGCTCTCAGAGCCGCACTTACTGAGCGCCGACCGCTGTT CAGGCGCATAGCTGACGCGTGGCGGGCAGACCCGCAACTTCTGAGCGCCGCGAGTGT AAAAGCGGACTCGTCTACCCCGTGTGTTTAGACCCAGCTCCCGTGAAGCTGCAGAG CACTCAGATCTGGACTTCGAGTCTGAGTCTGCTGCTCCCTTCAAGAGACTCAGGAGCAAGC GGTCACTCATCCATCTCCATCTCCAGGGGGGAACTCTCGGTGTGACAGTCTCAGCGTGTGG GTTCGGGATAGGACCCGCGACATCAAGGGCAGAGGAGGTGATGTTGTGGAGAGGTGAA CATTAACACAGTGTATCAACAGTCTTTTGAACCAAGTGGCGGACCAAACTCCGTTG ACAGCGGTGCGGGGCTTGACTCAAGCACTGGAAGTCTATGTTACCGAGTCAACCTTT GTCAAGCGCTGACCATGGATGGCAAGCGCTGCTGGCGTTTATCCGCGTAGAGTACGCGCTG TGTGTGTGCTCAGGAGAGGTGTGAGAGAGCTGTGACTGCGGACGCTCCCTCTCTGCTG CGCTCTTCACTCTCTCGGCGCCG	1001
NGFBu1	NGFB	G	C	-	-	noncoding	GE1186	TTTACAGAGA GCTGACGTTTG	GACAACAGCG TAACCCG	TTTACAGAGGAGCTGAGCTTTCCTACATCTACAAGTATGATAGGAGCTCCGCGGAGCGAGT GAGAGCCCTCCGAGGACGAACATACTCAACAATCTTGAACAAGTGGGGGATCATTTGTGG TG/CTAAGTGCAGTGGATGGAGTCTCTGGGACAGTATAGACCATCACTATTGATCA TGTCATCAATGAACAAACATAAAGAAAGACACTCTTAAGAGTGAAGAGAGAGGAGGGA GAAAGAGGAGGTGGATGAAGGACACTAGCTTAGAGGGTCAACTTGGATCTCATCTC TGGTTCAGTTTCTATTTGACTTCAGTCTTAGTGTAGTCACTTCTGTGAACAGTTCTC TTATATGTGAATAAATATGATAATCTTAATGAATCAAGACTCAAGAGATGAGAAGTGA ACCATTTAAAACATCACAAAGAGGAATATTATGTGGTCCCATTTATATATGTGGGTA GCGCTGAAGGTGCTGAGTGAAGTGTCCGAGCAAGGTTTTTGCACAACTACGACG TTGTGAATCTAACAAGGCTCCAGTCAAGATCTTAGAGCTGACCGAGTCACTGTCTGA AAGGGGTACCACTCTGAGGCTCAAGACATGCTCCCAAGATCTTCCCGTGCCTCCAGA GGATCAAAACTGTGAGCAGGAGCGCACTCAACATCAAGGCAAGTGGCGGAGGAGTGT AACTCTCCCAACACTCTCTGTACACATGGACACTTACCACCTCTCAGCGCTTAA GCTCAGAGACTCAAGGACTCTGAAGTGAAGTCTCAGCTCATCTCAACTCTGGGCAAA ATTCAGGGGCTCTGCTCTGCTGAGAGCTGGATGGGTGACCAACATCCATCTGCTG AGTCAAGCCGCGGTATACGCTCTTGTGTC	1002

FIG. 5A

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
NGFBu2	NGFB	A	G	-	-	noncoding	GE1186	TTTACAGAGGA GCTGACGTTTG	GACACAGGCG TAACCCG	TTTACAGAGGAGCTGACGTTTGCTACACATCTACAAGTATGCATAGGAGCTCCGCGGAGGCCAGT GAGAGGCCCTCCAGGAGCAGAACTAATCCCAATTAAGTACCAAGTTAGAGCCATCCCATTTGATCTATAGT GGTAAGTCAAGTCAAGTATGGAGTCTCTTGGGACAGTTAGAGCCATCCCATTTGATCTATAGT CACATAAGACAACAATAAAGAAAGAGACATGCTTAAGAGTGAAGAAAGGAGGAGGAGAA AGAAGGAGGAGTGGATGGAGGACACTAGCTTAGTAGGGTCAACTTGGATCTATCTCTGCT TCAGTTTCAATTTGACTTCAGTCTTAGTGTAGTTCACTTCTGTGAATCAGTTTCTCTAT ATGTAAATAAATATGATAAATCTCAATGAACTCAAGCTCATGAGAGATAGAGTGAAC ATTTAACAACATCACAAAGAGAACTATTATGTGTCACATTTATATGTGGGTAGCGT CTGAGAGTGCCTGGACTAAGATGTCCTCCAGAGCCAAAGTTTTCACCAATGAGCGTTTG TGAATTCATAACAAGGCTCCCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT AAGGGGTTACCACTTCAGAGGCTCAAGACATGCTCCAGCAGATCTCCCGTGCCTCTCGA GGATTCAAAAGTGTGAGCAGGACGACCATCACATCAAGGCAAGTCCAGTGCCTCTCCAG AAACTCTCCCAACCTCTCTGTTACACATGGACACTTACCACCTCCCTCAGCGCTTAA GCTTCAGAGAACTCAAGGACTCTGTAAGTGTCTCAAGTCTATATGAACTACTGGGCAAA ATTCAGGGGCTCTGCTCACTCTCTGAGAAAGTCTGGATGGGTTGACCACATCCCATCTGCTG AGTCAGGCCCGGTTACGCTCTGTTGTC	1002
NGFBu3	NGFB	G	T	-	-	noncoding	GE1186	TTTACAGAGGA GCTGACGTTTG	GACACAGGCG TAACCCG	TTTACAGAGGAGCTGACGTTTGCTACACATCTACAAGTATGCATAGGAGCTCCGCGGAGGCCAGT GAGAGGCCCTCCAGGAGCAGAACTAATCCCAATTAAGTACCAAGTTAGAGCCATCCCATTTGATCTATAGT GGTAAGTCAAGTCAAGTATGGAGTCTCTTGGGACAGTTAGAGCCATCCCATTTGATCTATAGT CACATAAGACAACAATAAAGAAAGAGACATGCTTAAGAGTGAAGAAAGGAGGAGGAGAA AGAAGGAGGAGTGGATGGAGGACACTAGCTTAGTAGGGTCAACTTGGATCTATCTCTGCT TCAGTTTCAATTTGACTTCAGTCTTAGTGTAGTTCACTTCTGTGAATCAGTTTCTCTAT ATGTAAATAAATATGATAAATCTCAATGAACTCAAGCTCATGAGAGATAGAGTGAAC ATTTAACAACATCACAAAGAGAACTATTATGTGTCACATTTATATGTGGGTAGCGT CTGAGAGTGCCTGGACTAAGATGTCCTCCAGAGCCAAAGTTTTCACCAATGAGCGTTTG TGAATTCATAACAAGGCTCCCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT GTTTGGGTTACCACTTCAGAGGCTCAAGACATGCTCCAGCAGATCTCCCGTGCCTCTCCAG GGATTCAAAAGTGTGAGCAGGACGACCATCACATCAAGGCAAGTCCAGTGCCTCTCCAG AAACTCTCCCAACCTCTCTGTTACACATGGACACTTACCACCTCCCTCAGCGCTTAA GCTTCAGAGAACTCAAGGACTCTGTAAGTGTCTCAAGTCTATATGAACTACTGGGCAAA ATTCAGGGGCTCTGCTCACTCTCTGAGAAAGTCTGGATGGGTTGACCACATCCCATCTGCTG AGTCAGGCCCGGTTACGCTCTGTTGTC	1002

FIG. 5BBBBBB

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence	
NGFBu4	NGFB	G	A	-	-	noncoding	GEL186	TTTACAGAGGA GCTGACGTTTG	GACAAACAGCG TAACCCG	TTTACAGAGGACGTTGCTACACATCTACAAGTATGCTAGGAGCTCCGCGAGGCCAGT GAGGCGCTCCAGGACGAGAACTAATCCCAATTAATCTAGCAAGTACCAAGTGGGGGATATATCTGTGG GGTAAGTCAGTCAGTATGAGTCCCTCTGGGGACAGTTAGGAGCACTGAGTATGATCTATAGT CACATAAGACAACTAATAAAGAAAGCATGCTTAAGAGTGAGGAGAAAGAGGAGGAGAA AGAGAGGGGTGGATGGAGGACACTAGCTTAGTAAGGGTCAACTCTGGATCTATCTCTGAT TCAGTTTCATTGTGACTCAAGTCTTAGTGTAGTTCTTCTGTAATCTATCTCTGAT ATGTAAATAATATGATAAATCTTAATGAACTCCAGACTCAGAGAGTGAAGATGAAGCAAC ATTTAAATAATCACAAAGAGGAATATATGTGTCCCACTTATATATGTGGGGTAGGCT CTGAGAGTGCCTGGACTAAGATAGTCCCAAGGACCAAGGTTTGTGCAAACTAGAGCTTTG TGAATCATCAAGGGGCTCCAGTCCCAAGTCTTAGAGCTGACCAAGTCACTGTCTGAAAGG GGGTACCACTCTGAGGCTTCAAGATCTCCCAAGCATCTCCCAAGAGATCTCCCTGTCTTCAAGAG TCAAACTGTGAGAGGACGACCATCATCAAGGACAAAGTCCGAGGAGAGTGA/ATGTT AAACTCTCCCAACACTCTGTGACACATGGAACATACCACCTCTCAAGCTCTCAAGCTCTAA GCTTCAGAGAACTCAAGGAACTCTGTAAGTGTGCTCCAAAGTCACTAGCACTACTGGGCAAA ATTCAGGGCTCTGCACTCTCTGGAGAAGCTGGATGGGTGACCAACATCATCACTGCTCTG AGTCAGCGCCGGGTTACGCTCTGTCTC	1002
NGFBu5	NGFB	T	C	V	A	cds	GEL185	CACATCCATAC TGCCTGAGT	AGGGGCCAGG AGAATG	CACATCCATACCTGAGTACGCCCGGTTACGGCTGTCTCCGTATCAACCATCTGCTAGCA CACCTTCTCCTCTCAGGAAGTGCCTGGTTTGAATGAACACTCTGCTGATCACTCTGGAGGCA ACTCTGAGGACCAAAACTGCTTTTGACTGCACTTAGTACTCAATGAATCACTCATCTTC TTTTCACTCCAGTGCATAGGTAATGTCCTGTTTCACTCTGATCAAGCTTTCTCTGA TCGGATACAGGCGGAACTACCTGAGAGCAATGTCCTGAGGACACACTATCCCAAGT /C/CCACTGGATAAACTTAGCATCTCCTTGACACTGCTCTCGAGAGCGCCGAGCGCCGG CAGCGGATAGCTGACGCTGCGGGGAGACCCGCAACTACTGTGGACCGCCAGCTGTTT AAAGGCGGCACTCTCTCACTGCTGTGTTTAGCACTCCAGCTCTCCGTCAAGCTGTCGA CACTCAGATCTGGAATCTGAGTCTGGTGTGCTGCCCTTCAACAGCACTCAAGAGCAAGC GGTCATCATCCATCCCATCTCCACAGGGGGAATCTCGGTGTGAGAGTCAAGCTGTGG GTGGGATAGAGCCACCACCAAGACATCAAGGGCAAGGTGATGGTGTGGAGAGGTGA CATCAACAAGTGTATCAACAGCTCTTTGAGACCAAGTGTGCGGGAACCACTCACTTTG ACAGCGGTGCGGGGATGTCAAGCACTGGAATCATTTGACCAAGCTCACTCACTCACTT GTCAAGCGCTGACCATGATGGCAAGAGGCTGCTGGTTTATCCGAGCACTCACTCTT TGTGTGTCTCAGCAAGAGGTGTGAGAAGAGCTGACCTGCTGCCGCAAGCTCTCCCTCCCTG CCCCCTCTACATCTCTGGGCCCT	1001

FIG. 5CCCCC

139/178

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
NGFBu6	NGFB	T	C	-	-	noncoding	GEL186	TTTACAGAGGA GCTGACGTTTG	GACACAGGCG TAACCCG	TTTACAGAGGAGCTGACGTTTGTCACATCTACAAGTATGATAGAGTCCGCGGAGGCCAGT GAGAGGCTCCGAGGAGAGAACTATCCCAATTAAC/CCTGACCAAGTGGGGATCATTT GTGGGTAACTGCGAGTATGAGTCCCTCTGGGACAGTATAGCCATACCATTTGATCTA TAGTCATAGAACAACAATAAAGAAAGACATGTTAAGAGTGAAGAGAAAGGGAGGGA GAAAGAGGAGGGTGGATGGAGGACACTAGCTTAGTGGGTCACCTTGGATCTCTATTC TGGTTCAGTTTCTATTGTGACTTCAGTCTTATGTTAGTTTCAATTTCTGGAATCAGTTTC TATATGTAAATAAATATGATAAATCAATTAATGACTCAGACTGATGAGAGATGAGTGA ACACATTTAAACAATACACAAGAGGAACTATATGTGATCCACATTTATATATGTGGGTA GCTCTGAGAGGTGCTGACTGAAGATGGTCCAGAGCCACAAGTTTTCACAACATGACGC TTGTGAATTCATAACAAGGCTCCCAAGTCCACAGATCTTAGAGTGACCCGACTGCTGGA AAGGGGTACCACTTCTGAGGCTCAAGACATGCCCCAGAGATCTCCCTGCTCTCCAGA GGATCAAAACTGTTGAGCGAGGACGACCATCACATCAAGGACAAGTCCAGGAGAGGTGT AACTCTCCCAACCACTCTCTGGTACACATGGACACTTACCACCTCCAGCGGCTTAA GCTTCAGAGAACTCAAGGACTCTGTAAAGTGTGCTCCAAGTCTATCGAAGTCTGGGCAAA ATTCCAGGGGCTCTGCTCACTCTCTGAGAGAGTGGATGGGTTGACCAACATCCCATCTGCTG AGTCAGCCCGGGTTACGCTTGTGTC
NGFBu7	NGFB	C	T	-	-	noncoding	GEL186	TTTACAGAGGA GCTGACGTTTG	GACACAGGCG TAACCCG	TTTACAGAGGAGCTGACGTTTGTCACATCTACAAGTATGATAGAGTCCGCGGAGGCCAGT GAGAGGCTCCGAGGAGAGAACTATCCCAATTAAC/CCTGACCAAGTGGGGATCATTTGG GTAACTGCGAGTATGAGTCCCTCTGGGACAGTATAGCCATACCATTTGATCTATAGT CACATAGAACAACAATAAAGAAAGACATGTTAAGAGTGAAGAGAAAGGGAGGGA AGAAGAGGGTGGATGGAGGACACTAGCTTAGTGGGTCACCTTGGATCTCTATTCGT TCAGTTTCTATTGTGACTTCAGTCTTATGTTAGTTTCAATTTCTGGAATCAGTTTCCTAT ATGTGAATAAATATGATAAATCAATTAATGACTCAGACTCATGAGAGATGAGAGTGAACAC ATTCAAAACCTCAACAAGGAGGAGTATTTGTTGCTCACTTATATATGTGGGTAGCGT CTGAAGGTGCTGGACTAAGATGGTCCAGAGCCACAAGTTTTCACAACATGACGCTTGT TGAATTCATAACAAGGCTCCAGTCCAGATCTTAGAGTGACCCAGTGCAGTCTGTGAAGG GGTATCCAGTCTGAGGCTTCAAGACATGTCACAGAGATCTCCCTC/TGTGCTTCCAGA GGATCAAACTGTTGAGCGAGGACCACTCACATCAAGTCCAGGAGAGGTGTT AACTCTCCCAACCACTCTCTGGTACACATGGACACTTACCACCTCCCTCAGCGCTTAA GCTTCAGAGAACTCAAGGACTCTGTAAGTGTATCTCCAAGTCTATCGAAGTCTGGGCAAA ATTCCAGGGGCTCTGCTCACTCTCTGAGAGAGTGGATGGGTTGACCAACATCCCATCTGCTG AGTCAGCCCGGGTTACGCTTGTGTC

FIG. 5DDDDDD

[illegible]

FIG. 5EEEEEE

[illegible]

FIG. 5FFFF

[illegible]

[illegible]

[illegible]

FIG. 511111

[illegible]

FIG. 5JJJJJ

[illegible]

FIG. 5L1L1L1L

FIG. 5MMMMMM

[illegible]

FIG. 5NNNNNN

[illegible]

FIG. 5000000

[illegible]

FIG. 5Q-Q-Q-Q-Q

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
PCId17	PCI	C	T	N	N	cds	GE413	GGACATCTCTG GAAAGTCAGC	TGAGGGAAATTG GGTATTCTTTA GAT	GGACATCTCTGGAAAGTCAGCacctggaccagctccaccctctctgaggacacactcttttccctt ttcagacaagaagacacacacatgcagctcttctctctctgtgctctgtgctcttcacgacctc aggggcctcccttcacgccacacacccggagatgaagaagagtcgaggacctccatgata ggtagccagtgccccccagacagaggagactttacctttgacctacagaccttggctttc cgctcccccaggccagaa [c/t] atcttttcccccttgagcatctccaagacctggcccatg ctctccctgggggctggg tccagacaagaatgcagatcctgggggctggggctcaacctcca gaaaagctccgaagagagctgcacagagctttcagcagctcttcaggaaactccacacccca gagatggcttccagctgagctcgcaatcttttcacggaccttggggtagacctgcaggac accttcgtaatggccatgaagacctgtaccttgcgcagacacttcccccaacctttaggagctc tgcaggggccatgaagcagatcaatgatattgtggcaagaacagaggccaagattgtggact tgccttaagaacctcgatagcactcgctgcatgctggaattacatctctcttaaaaggtaa ggccttggggcccaaaactgcactttctttgggttttctgtgcttttctTAAAGNATACCCAAAT TCCCTCA
PCId18	PCI	C	T	P	P	cds	GE413	GGACATCTCTG GAAAGTCAGC	TGAGGGAAATTG GGTATTCTTTA GAT	GGACATCTCTGGAAAGTCAGCacctggaccagctccaccctcttgcaggacacacttttccctt ttcagacaagaagacacacacatgcagctcttctctctctgtgctctgtgctcttcacgacctc agggggctcccttcacggccacacccggagatgaagaagagtcgaggacctccatgata ggtagccagtgggccccccagcagaggagactttacctttgacctacagaccttggctttc cgctcccccaggccagaa [c/t] ctctcccttgagcatcttcacacctggggcctggccttgcct ccctgggggctgggttcagacacaagatcgatcctggagggctggggctccacctccagaaa agctcagagaagagctgcacagagctttcagcagctcttcaggaaactccacacccagaga tggcttcagctgagctcgcaatgccttttcacgaccttggtagacctcagacctgagacact tgcataagtcctgaagcgtgtacctggcagacacttccc [c/t] accaactttaggagctc tgcaggggccatgaagcagatcaatgattattgtggcaagaacacagaggccaagattgtggact tgccttaagaacctcgatagcactcgctgcatgctggaattacatctctttaaagggtaa ggccttggggcccaaaactgcactttctttgggttttctgtgcttttctTAAAGNATACCCAAAT TCCCTCA
PCId1	PCI	T	C	F	F	cds	GE413	GGACATCTCTG GAAAGTCAGC	TGAGGGAAATTG GGTATTCTTTA GAT	GGACATCTCTGGAAAGTCAGCacctggaccagctccaccctcttgcaggacacacttttccctt ttcagacaagaagacacacacatgcagctcttctctctctgtgctctgtgctcttcacgacctc agggggctcccttcacggccacacccggagatgaagaagagtcgaggacctccatgata ggtagccagtgggccccccagcagaggagactttaccttt [c/t] gacctacagggctctgg ctctccctggggctgggttcagacacaagaatgcagatcctgggggctggggctcaacctcca gaaaagctcagagaagagctgcacagagctttcagcagctcttcaggaaactccacacccca gagatggcttcagctgagctcggaatgcctttcaccgaccttgggttagacctttaggagac accttcgtaatggccatgaagacctgtaccttgcgcagacacttcccccaacctttaggagctc tgcaggggccatgaagcagatcaatgattattgtggcaagaacacagaggccaagattgtggact tgccttaagaacctcgatagcactcgctgcatgctggaattacatctctttaaagggtaa ggccttggggcccaaaactgcactttctttgggttttctgtgcttttctTAAAGNATACCCAAAT TCCCTCA

FIG. 5RRRRR

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
PCIu10	PCI	G	C	G	R	cds	GE394	TGGCTATCTTT ACTGTCTTCAC TCC	GTCTTTGCCAC CAGTGTGT	TGGCTATCTTTGATTCCTCTCTTTATTTGAGCTGAGAAATTTCTAAATCTTGACAAAAAT TCTTTTCATTTTCTCTTTTTCATCTTTAGCTAAGTGGAGACAGCTCTCAACCAAAAG/C TGCACCAAGAGCAAGACTTCACTGAGCTCGGAGACTTGGTGGGATCACTCATGAGCCG CAGGATCATCATCACTCACTCCCTGAGCCAGAACTCTCTGCAAGGTTGGTGGGTTCTCTTACC AAGGCAATGCCACCGCTTTGTTCATCTCCCACTGAGGAGAGATGCAAGCATGGAGAAATGGA CTGAGTGGAAAAACGCTGAGGAAGTGGCTTAAGATGTCAAAAAGAGGTACTTTCAGACTACCC AGGGCCAGCTCAAAACCAACAGCAGCCAGGAGACACACACGCTCTACCAGGGCCACACAGCACT GTGGGAGGAGAC
PCIu2	PCI	A	G	N	S	cds	GE413	GGACATCTCTG GAAAGTCAGC	TGAGGGAATTG GGTATTTCTTTA GAT	GGACATCTCTGGAAAGTCAGCACTGGACAGCTCCACCTCTCTGAGGACACACTTCTTCTCT TTCAGACAAAGACAGCAACCATGCAAGCTCTCTCTCTCTCTGTGCTGTGCTCTCAAGCCCTC AGGGGGCTCTCTCTCAAGCCACACCCCGGAGATGAGAGAGAGTCAGGAGCTCTCATGTA GGTGCACGGTGGCCCCCAGAGCAAGAGGACTTACCTTGGACTTCAAGAGCTCTGCTCTCT CGTCCCCCAACCAAG/A/GTCATCTTCTCTCTCTGGAGCATCTCCATGGAGCTCTGGCTCT CTCTCTGGGGCTGGTCCAGACAAAGATGCAATCTCTGAGGAGCTGGAGGCTGGAGCTCAAGCTCCA GAAAGCTCAGAGAGAGAGCTGCACAGAGCTTTCAGCAGCTCTTCAGGAACCTCAACAGAGCCCA GAGATGGCTTCAGCTGAGCTCGGCAATGCCCTTTCACGCACTGGTGGAGACTCGAGGAC ACCTTGTAAAGTCCATGAAGAGCTGTACCTGGCAGACACTTCTCCCAACCACTTLAGGAGACTC TGCAGGGGCAATGAGCAGATCAATGATTATGTGGCAAGCAACAGAGGGCCAGAGTATGGAGCT TGCTTAAGACCTCAGTCAAGATCGTGTGATCATGTGAATACATCTCTCTCTTAAAGGTAAG GCCCTTGGGCCAAACCTGACTTCTTGGCTTTCTGTGCTTTTATCTTAAAGAAATATCCCAAT TCCCTCA
PCIu3	PCI	C	A	I	I	cds	GE375	GAAAGCTTGCC ATTTCCTATG	GTGTGGGTGGA AGCAATCA	GAAAGCTTGCCATTGCTATGATGACTTCACTGCCCCCTGGTGGCTTGGTGTGCTCGTCTC CCCTGAGATGTCACAAAGCTGTGTGGAGTGGACGAGTCGGGAAACCAAGCAGCGAGCC ACGGGACAAT[C/A]TTCATCTTCAAGTCCGCCCTGAATCTCTCAGAGCTAGTGTCTCAACA GGCCCTTCTGATGTCAATGTGGATAACAACATCTCTCTTGGCAAGATGAACCGCCCTGA GGTGGGCTTCTCTGAAATCTCAAGGCTCAAGGTTGGGAGATGAGAGGGGCTATGCTATGGCCC ATCTGATGCTGGTGTAGTGTATTACAGAGGTTTGTGTGACTAGATGAGGACATCAACAATAA TATTACTCTATGGAATGATTGCTTCCACCCACAC
PCIu4	PCI	G	A	S	S	cds	GE375	GAAAGCTTGCC ATTTCCTATG	GTGTGGGTGGA AGCAATCA	GAAAGCTTGCCATTGCTATGATGACTTCACTGCCCCCTGGTGGCTTGGTGTGCTCGTCTC CCCTGAGATGTCACAAAGCTGTGTGGAGTGGACGAGTCGGGAAACCAAGCAGCGAGCC ACGGGACAATCTTCACTTTCAGTGC[A/G]GCCGCTGAATCTCTCAGAGCTAGTGTCTCAACA GGCCCTTCTGATGTCAATGTGGATAACAACATCTCTCTTGGCAAGATGAACCGCCCTGA GGTGGGCTTCTCTGAAATCTCAAGGCTCAAGGTTGGGAGATGAAGGGGCTATGCTATGGCCC ATCTGATGCTGGTGTAGTGTATTACAGAGGTTTGTGTGACTAGATGAGGACATCAACAATAA TATTACTCTATGGAATGATTGCTTCCACCCACAC

FIG. 5SSSSS

FIG. 5TTTTT

[illegible]

FIG. 5UUUUU

[illegible]

FIG: 5VVVVV

[illegible]

[illegible]

FIG. 5XXXXXX

[illegible]

FIG. 5YYYYYY

FIG. 5ZZZZZZ

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
SELPrd2 4	SELP	C	T	P	L	cds	GE954	TGCCACCCCT GNAAGT	GGGCTGGGCT GTCCAT	TGCCACCCCTGAAGATTctctgaacgaggaaacatgatctgccttctatcttcgaaaagcattccca gcatcgtctcagctgcagcttcagttgtgaaggagatttgcatagttggac (c/t)ggaaagt gtagcatgacacgacctcgggggtATGACAGCCCGCC
SELPrd2 5	SELP	G	A	V	M	cds	GE446	CTCTGTCAGTG AGAGAGTG	CACGTGTGGAGG CTATTG	CTCTCTGAGTCAGAGATgtggagaacttgagctctctctcaacac (g/a)tgctcatgaactgcag ccacctctggaaactctctcttcttaactcgcagtgcaagcttcctcactgcacgaggtaccgaag taaatgggcccacgaagctggaaagtcttggtcttggaatctggacCAATATAGCCTCCACAGTG
SELPrd1	SELP	A	C	N	T	cds	GE462	TACTCTAGCCA TCAGTCCC	ATATTATTACC TTTCAGGTTG	TACTCTAGCCATCAAGTCCcagaactctttgcccaacgagcagcttgatattcttgaca ctctgtggagaattcaatgttgcttcacactgcatctctctgtgaaca (a/c)tgctcttaagct ggaggggcccaataatgtggaatgcacaactctggagaatggctcagctactcccaCAACTGCA AAGGTAAATAT
SELPrd1 0	SELP	A	G	T	A	cds	GE466	TCTCTCCAGCT GTGCAGT	AAATCTTACC CTCACAGG	TCTCTCCAGCTGTGCAGTgtcagcactctggaagcccccagctgaagga (a/g)ccatggaacttgt tcatcgcctcactgcttttgcatatggctcagctgcaaatcttggaatgccagccggtctacagag tgaggggcttggaactgctcgcctgcatgaecttggaactggctgcacaccttgccaaCCTGT GAGGTAGGATTTT
SELPrd1 1	SELP	T	C	T	T	cds	GE462	TACTCTAGCCA TCAGTCCC	ATATTATTACC TTTCAGGTTG	TACTCTAGCCATCAAGTCCcagaactctttgcccaacgagcagccttgatattcttgaca c (c/c)ctgtggagaattcaatgttgctcacaactgtctctctgtgaacaatggctttcaagct ggaggggcccaataatgtggaatgcacaactctggagaatggctcagctactcccaCAACTGCA AAGGTAAATAT
SELPrd1 2	SELP	A	G	N	D	cds	GE462	TACTCTAGCCA TCAGTCCC	ATATTATTACC TTTCAGGTTG	TACTCTAGCCATCAAGTCCcagaactctttgcccaacgagcagccttgatattcttgaca ctcgtggagaattcaatgttgcttcacactgtctctctgt (a/g)acaatggctcttaagct ggaggggcccaataatgtggaatctctggagaatggctcagctactcccaCAACTGCA AAGGTAAATAT
SELPrd1 3	SELP	A	G	T	T	cds	GE421	TTTGTACAGG ACCATTGA	TCTTTATTACC TTCTTCTGTA	TTTGTAGGCACCATTTGActalccaggaaagccctgacttactcttggtggagggctggctctac (a/g)ataggctcgataatgggtgggagctctcctgctgtgctgaagaagcgtttTCACAAAA GGTAAATAGGA
SELPrd1 4	SELP	G	A	P	P	cds	GE483	AACGAGAAGA ACGTGCAG	AAGGCTCTACC TGTGTAA	AACGAGAAGAATGGAGGatcggacttatcatcacgacacaaagcatactctggaatatttc cgtgaataactgacgaatcgtctacagacttagtggtccatccagacaaatctgaaatctgatt acctcaataaggtctacctctactcactgctcactgattggtatcggaagacgaataag acatgacatgggtgggaacaaagagctctcaccacagggcttgagaactgggctgataatga acctaacacaaaggaacacacgaggactcgtggtggagatatacatcaagagctc (g/a)tcagcc cttggcaagtggaaatgatgagcactgcttgaaagaaaagcagcatctgtgtTACACAGGTAGGGC CTT
SELPrd1 5	SELP	T	C	F	S	cds	GE466	TCTCTCCAGCT GTGCAGT	AAATCTTACC CTCACAGG	TCTCTCCAGCTGTGCAGTgtcagcacttgaaagcccccagtgaaaggaacatcggactgtgtcat ccgctcactgctt (t/c)tgcatatggctcagctgcaaatcttggtgtgccacccggtctacagag tgaggggcttggaactgctccgctgcatctggacattggactgtgacaccttgccaaCCTGT GAGGTAGGATTTT
SELPrd1 6	SELP	C	T	S	F	cds	GE445	ATCCCTTAGCT TTGCAGTG	ACACTCTTACC TTGGCATTC	ATCCCTTAGCTTTTGCAGTGccaggatctccagctcccaaatcgaagcccccgggtgaaactctccac cccttcggtgctcttaggcacacagctcagctcagctcactcgaatgaagaggtctgctcgtgt ggagcaaggtgctcagcttgcttggtcactggaaactggaaat (c/t)tgctctccgaAAATGTC CAAGGTAGAGTGT

FIG. 5CCCCC

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
SELPU5	SELP	T	G	L	V	cds	GE451	TCACACAGC ATAGCAT	CTCTTCATGC TGGAGTT	TCACACAGGCATGACATCACTTCTCTACTCCAGG T/g Tgcagtgtccagccctcaccactcc tgggcagggaaccatgtactgtaggcatcatccgggaacctttggttttaataaccacttggtaact ttggctgcacgctggattcacaactcatatgagagacagcaactctcagctgcagaccttcaggagaa tggaaagcagc A/CTCACACATGCCAGG
SELPU6	SELP	A	G	H	V	cds	GE466	TCTCTCCAGCT GTGCAGT	AAAATCCTACC CTCACAGG	TCTCTCCAGCTGTGCAGTGTGAGCACTGTGAGCCCCAGTGAAGAACCATGGAGCTgttcat cgcctcactgcttttgcctatgtgtccagctgcaaat tgatgtccagccggcttcagagtgtag gggcttggac a/g TgctctgtcactctggacactctggacactggctctggcaaccttgcgaacctCTGT GAGGTGATGTTTT
SELPU7	SELP	T	C	C	C	cds	GE462	TACTTAGCCA TCAAGTCC	ATATTATTACC TTTGCAGTTG	TACTTAGCCATCAAGTGGCCAGAACTcttgcaccagagcaggcagcctggattgtttgaca ctcgtggagaattcaatgttggctccacttg c ctattctcttgacaattggcttttaagct ggagggcccaataatgtggaaatgcacaactctgggaagtggctgagctactcccaAACCTTCCA AAGTAAATATAT
SELPU8	SELP	A	C	T	P	cds	GE452	CAGCTGTGAAA TGCTCAGA	AAAATTGTACC TTTGCCAGG	CAGCTGTGAATGCTCAGAACTacactgtttaaagccaatagcagatgaactgctcccaactctgg ggaaactcagttatggatcaactgtctcttcttccatgtctcagagggccagttacttaattggctc tgcaacaacagcatgccaaagaaatggccactgg a c ctacgtgtcccaacttctccAACCTTCCA ACAATTT
SELPU9	SELP	A	T	K	*	cds	GE483	AACGAAAGCA AGTGGCAG	AAGGCCCTACC TGTGTAA	AACGAAAGAGTGCACAGatggacttatcattcaagacacaaagcatcataatggaaattcttc cgt a l aatactgccagaatcgtcacagagacttattggctccatccgaataaataatgaatt gatctactcaataaggtctctactcactcagctctactactggtttggatccgaagaagacaa taagcatggcatgggtgggaacaaaaaggtctctaccaagaggtc gagaagctggagctgata atgaacctaacaaaggaacacaggaactgcgtggagatgacatcagagtcgltcagcc cctggcgaagtggaa gatgagcactgcttgaagaaagacgcgattgt TTACACAGGTAGGGC CTT
SHBGd3	SHBG	T	C	-	-	noncoding	GE539	TGACATGTCCC TACTACGTTT	AACCAGGGAC TGGGTC	TGACATGTCCCTACTCAGCTTgtttgt c t ctctctctctgtatagagtgtccacagaccctcc ggctgtccactcagcaatggccaggacagagcctatcgtctctgtatgaactttgacctcaacca agatcacaaaglatgggg tggcctagcctctGACCCAGTCCCTTGGTT
SHBGd4	SHBG	C	T	P	L	cds	GE603	GCCAGAACAG ATCCCAAG	CCAGCAGTCT TTACCAAGTC	GCCAGAACAGATCCAGGgctctgtattgttctccactctctcaggtggagagctcaagat ggaggggactctgtctgtcaggtggatggagagagctgtcgtcgtcagcagagctctcgt ggccctgaccacaaacgcctccatcataggaat tgagct gggggggctgctctcccccgt tccaactctgggttgc c t ggtaactacaccccggggtggaaacctcagccaagctTGTGTAA AGCACTGCTGG
SHBGd5	SHBG	G	A	D	N	cds	GE605	CACCTTAATGC TCTTAATCCA	TGCTTAGTCCA CAGTGAATATT TG	CACCTTAATGCTCTTAATGCCACctttggactacctctctcctcaggagaa g a actcttccact cttttggctgaatggcctttgggacaaggctcagagctggatggctggccggccttgaaacaga agccatgagatcggactcagagctggccagcagccagcagcagcagcagcagcagcagcagcagc aagctccacttaagaacccctttgaaagtactgattattcatttcaacaaATAATTCAT GTGCACTAGCAA
SHBGd6	SHBG	C	A	T	N	cds	GE605	CACCTTAATGC TCTTAATCCA	TGCTTAGTCCA CAGTGAATATT TG	CACCTTAATGCTCTTAATGCCACctttggactacctctctcctcaggagaaagactcttccacactctt tgcctgaatggccttgggacaaggtcagagctgagatgtggaccggccttgaaacagac atgagatggat c a t cagcgtctcccgagcagcagcagcagcagcagcagcagcagcagcagc aagctccacttaagaacccctttgaaagtactgattattcatttcaacaaATAATTCAT GTGCACTAGCAA

FIG. 5EEEEEE

[illegible]

FIG. 5FFFFF

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
SLC6A1 u5	SLC6A1	C	A	I	I	cds	GE1097	AGGAGAGGGG TCACCAAGT	CTGTGTTTACA GTGAGGGTCA	AGGAGAGGGGTACACAGTcaaccactttctctccagggtggtctacttttcagccacataccctt acat(c/a)atngctgmatcactctncttctcttgatgagtcgagctgcgccggggcccaagagggg cactcttttacaacacacccaactccgcaagctgtctgactccgggtgagtcgccctccca gccggattctgagccaccacttagcagcttgagataagcttttgactcttttTGACCTCACT GTGACCAAG
SLC6A1 u6	SLC6A1	G	T	T	T	cds	GE1078	CGGCTCCAC CAGCTC	CTGTGTTCTTT ATCAGTGCC	CGGCTCCACCAAGCTCTgtgaactttctctctctccactgtttgaccaggcgcaacatgcatt cagatagagcctgggataagcaggccagatccgtggtccactggccactggccacac(g/t)ctgg ccattcgctggatcctgtgtattcttgatctgggaagggttggtgtgagctggaaaggaag gatatgtgcacagtggggacagagGCATCGATTAAAGAACACAGG
SLC6A1 u7	SLC6A1	T	A	I	N	cds	GE1044	AATTCCCTATT AATTGGAGC	GTGGTCTTTGT TGGATGGG	AATTCCGATTAAATGGACGngggttgtgtctcgtccagggctggggccttgggctgtcgtgtg acatctctgttgatgaacatctactaca(c/a)tgatcattctctgtggccatcttactacctgt ccaatctctccaccgggtgagtggtctacttttgaccctcccaTTCACAAAAACAC
SLC6A1 u8	SLC6A1	G	C	C	S	cds	GE1250	GCAGACACTGC CTGGA	CTCTGTCGGG CTCTGG	GCAGACACTGCGTGGAAacagtgcgaacaccttggaacacagaccgt(g/c)ctctccaac tacagatggttcaacactaccacatgaccagcctgtgtggtagtcttgaggagtgagtagtgga ctaatcgaggatggcaggagggggcatctcagcKAGAGCCCGAGGAG
SLC6A3 dl3	SLC6A3	G	A	R	Q	cds	GE1045	TGCAGACGTGG CTGTCT	CCCATGTCTTAC AGGCCCAAT	TGCAGACGTGCGTGTGcactccacagacagcatgcatacagacactggggcctctccaggggc gtggcagctcacagcctgagctgtgtgtgctatgctgtctctacttcagcctcttggaagggc gtgagcactcagggaagggtgagctgggggtccaccaATTGGGCTGTGACATATGG
SLC6A3 dl4	SLC6A3	G	A	V	M	cds	GE1128	TGAAGACCAAG AGGGAG	CTTACGCCAC CATTTT	TGAAGACCAAGGGAagacagaaatctctcaactccagtggtcccatgagtagaagacaaa tgcctcgtgggaactcatgtcttcgttggtggccccggctaaaggccccaaatgccgtgggcccgaagggtggagctcatctgtctcaaggagacagaggtgcagctcacagctcacccctccaca acccggcagagcccc(g/a)tggaagcccagagatcggaagacctggggaacaaagatcgactt tctctgtcgtcatgtgcttctgtgtggactggccaaagctgtggcggttccccctacctgtct acacAAATATGTGGCGGTAG
SLC6A3 u1	SLC6A3	C	G	L	V	cds	GE1045	TGCAGACGTGG CTGTCT	CCCATGTCTTAC AGGCCCAAT	TGCAGACGTGCGTGTGcaactccacagagacatggcatcgacagacctggggcctctccgggtg gga(g/c)gtcacagcctgctgtgtgtgtcatcgtctactctacttcagcctcttggaagggc gtgaagacctcagggaagggtgagctgggggtccaccaATTGGGCTGTGACATATGG
SLC6A3 u10	SLC6A3	G	T	P	P	cds	GE1128	TGAAGACCAAG AGGGAG	CTTACGCCAC CATTTT	TGAAGACCAAGGGAagacagaaatctctcaactccagtggtcccatgagtagaagacaaa tgcctcgtgggaactcatgtcttcgttggtggccccggctaaaggccccaaatgccgtgggcccgaagggtggagctcatctgtctcaaggagacagaggtgcagctcacagctcacccctccaca accc(g/t)cggcagagccccgtggagcccgagatcggaagacctggggaacaaagatcgactt tctctgtcgtcatgtgcttctgtgtggactggccaaagctgtggcggttccccctacctgtct acacAAATATGTGGCGGTAG
SLC6A3 u11	SLC6A3	C	A	L	I	cds	GE1045	TGCAGACGTGG CTGTCT	CCCATGTCTTAC AGGCCCAAT	TGCAGACGTGCGTGTGcaactccacagagacatggcatcgacagacctggggcctctccgggtg gga(g/c)gtcacagcctgctgtgtgtgtcatcgtctactctacttcagcctcttggaagggc gtgaagacctcagggaagggtgagctgggggtccaccaATTGGGCTGTGACATATGG
SLC6A3 u12	SLC6A3	G	C	V	V	cds	GE1045	TGCAGACGTGG CTGTCT	CCCATGTCTTAC AGGCCCAAT	TGCAGACGTGCGTGTGcaactccacagagacatggcatcgacagacctggggcctctccgggtg gga(g/c)gtcacagcctgctgtgtgtgtcatcgtctacttcagcctcttggaagggc gtgaagacctcagggaagggtgagctgggggtccaccaATTGGGCTGTGACATATGG
SLC6A3 u12	SLC6A3	G	C	V	V	cds	GE1045	TGCAGACGTGG CTGTCT	CCCATGTCTTAC AGGCCCAAT	TGCAGACGTGCGTGTGcaactccacagagacatggcatcgacagacctggggcctctccgggtg gga(g/c)gtcacagcctgctgtgtgtgtcatcgtctacttcagcctcttggaagggc c agacacctcaagggaagggtgagctgggggtccaccaATTGGGCTGTGACATATGG
SLC6A3 u12	SLC6A3	A	G	I	V	cds	GE1043	CAAGGGCCCTG CCTTGG	ACAGAGCCCTC GCAGAGC	CAAGGGCCCTGCTTGTGcagccttggtgacactgtctctctcaggttggtatag(g/a)gtcaaca gccacatggcatcagctgtctcactcagctgtcgtcgtgggtgagctcactctggagacct aaacgaactcaaacatctcaactctcaactctcaagcgtctgagcgtGTGAGACACCTGCT

FIG. 5GGGGG

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
SILC6A3 _{u3}	SILC6A3	G	A	S	S	cds	GE990	TCAGGCGCCAGG GCTGAT	CACGGCGCTGT CGATAC	TCAGGCGCCAGGCGCTGATATTCATCATCTATCCCGGAAGCCATCGCCACGCTCCCTCTGTCTCTG
SILC6A3 _{u4}	SILC6A3	C	T	A	A	cds	GE1043	CAAGGCGCCCTG CCTGTG	ACAGAGCGCTC GCAGAGC	CAAGGCGCCCTGCTGTCAGAGCTGTGACACTGTTCTCTCTCTGAGGTGTATGATGATCAGAGC
SILC6A3 _{u5}	SILC6A3	C	T	A	A	cds	GE1273	CTTTGCTCTGG CACCGC	AGCCTTCTGG TGCGCTCA	AGAGCGGCTCAGAGCATACAGGCTGTGACCTTCTACCGGCTCTGTCGAGGCGCTGTCT
SILC6A3 _{u6}	SILC6A3	C	T	N	N	cds	GE1128	TGAAGACCAG AGGGAG	CTTACCGCCAC CATTTT	CTTTGCTCTGACACCCGCTGAGAGCTGTGACCTTCGATATCTGTGGTGTGAGTCTGGGTG
SILC6A3 _{u7}	SILC6A3	C	T	P	P	cds	GE1128	TGAAGACCAG AGGGAG	CTTACCGCCAC CATTTT	CTTTGCTCTGACACCCGCTGAGAGCTGTGACCTTCGATATCTGTGGTGTGAGTCTGGGTG
SILC6A3 _{u8}	SILC6A3	G	C	R	R	cds	GE1128	TGAAGACCAG AGGGAG	CTTACCGCCAC CATTTT	CTTTGCTCTGACACCCGCTGAGAGCTGTGACCTTCGATATCTGTGGTGTGAGTCTGGGTG
SILC6A3 _{u9}	SILC6A3	C	G	A	G	cds	GE1128	TGAAGACCAG AGGGAG	CTTACCGCCAC CATTTT	CTTTGCTCTGACACCCGCTGAGAGCTGTGACCTTCGATATCTGTGGTGTGAGTCTGGGTG
SILC6A3 _{u10}	SILC6A3	A	C	K	N	cds	GE1113	CATCTCTATCT GAGTGGATATT GT	TTTCTCCCAA AACAAATAGTA GTC	CTTTGCTCTGACACCCGCTGAGAGCTGTGACCTTCGATATCTGTGGTGTGAGTCTGGGTG
SILC6A3 _{u9}	SILC6A3	G	A	T	T	cds	GE1071	TGTGACATCTT TCTAGGACAGG T	CTTCTTTTCT CTTCAATCC	CTTTGCTCTGACACCCGCTGAGAGCTGTGACCTTCGATATCTGTGGTGTGAGTCTGGGTG

FIG. 5 HHHHHH

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
SLC6A4_u1	SLC6A4	G	C	K	N	cds	GE1124	CGTTGGGCCCA CCCTTA	TGGCCTTGCCCC TAACAGG	CGTTGGGCCACACCTTAaactcgccctctgtctctccatcttccatcttaccactgcccaggagattgggtatgcccattcgatcattgccttttaccattgtctctactacacacattatcgcttggcctggcctat actgactatctctcttcacgacagctgcccctggacagctgcac g/c aactctctggaa cactggacactgcaccaattactcttcgaggagacacattcacttggacctccattctcacgtccc ctgctgaagaattttacacgcgcacgttaagtcacgttaagtgagggttgccCTGTATTAGGGGCGCAGG CCA
SLC6A4_u2	SLC6A4	C	A	-	-	noncoding	GE1027	AGCATCAGTAA CCTGCACACTC	ATTTCGAAGCC CGACTGGT	AGCATCAGTAACTGCACACTCTctctctcttaggtctctctggaggaagcgaccttgccttgccctctgattgcagaataacaggggcttaagggACCACTGGCGCTTGCNAAT ctaggtagcagcagggaagtttaaggACCACTGGCGCTTGCNAAT
SLC6A4_u3	SLC6A4	A	C	-	-	noncoding	GE1027	AGCATCAGTAA CCTGCACACTC	ATTTCGAAGCC CGACTGGT	AGCATCAGTAACTGCACACTCTctctctcttaggtctctctggaggaagcgaccttgccttgccctctgattgcagaataacaggggcttaagggACCACTGGCGCTTGCNAAT ctaggtagcagcagggaagtttaaggACCACTGGCGCTTGCNAAT
SLC6A4_u4	SLC6A4	G	C	G	A	cds	GE1145	AAATCCAAAGCA CCACAGAT	ACTCCGGGTCA CAGCCAC	AAATCCAAAGCACCCAGAGATcaattgggactcttggcagatggacacatcagttcatttactaaccc agcaggatggagacgcgccttgaaattctcagaagcagctatcacggctgaagatgggaaga tctgcaggaataacggagttctacagagggtctgtcccccacggggacagaaggagctccggg aaatatcaattgggtactcagcagttcccaagcttggtcggg g/a agatgacacacgcactc tatcccgacacacacacacactagttggctgactctcaagggaagcggagacactctgggga agaagggtgattctctctctcagttatggctatgctgtgagcctggcagatgctggcgtctc ccctacatattgttaccagaatggagggggtcagatcacagcgtgcagatagtggtctgaacca ggGTGGGCTGTGACCCCGAGT
SLC6A4_u5	SLC6A4	G	C	M	I	cds	GE1124	CGTTGGGCCCA CCCTTA	TGGCCTTGCCCC TAACAGG	CGTTGGGCCACACCTTAaactcgccctctgtctctccatcttaccactgcccaggatgggttatgcccattgcacattgccttttaccattgtctctactacacacattcat g/c gcccggggg ctactactcattctctctcttcacggccagctggcctggaccagctgcagaactctctggaa cactggcaactgcaccaattactctcggagacacattcacttgcacctccattctccactctcc ctgctgaagaattttacacgcgcacgttaagtcacgttaagtgagggttgccCTGTATTAGGGGCGCAGG CCA
SLC6A4_u6	SLC6A4	C	T	F	F	cds	GE1124	CGTTGGGCCCA CCCTTA	TGGCCTTGCCCC TAACAGG	CGTTGGGCCACACCTTAaactcgccctctgtctctccatcttaccactgcccaggatgggttatgcccattgcacattgccttttaccattgtctctactacacacattcatggcctggcctgcat actactctatctcttcacggccagctgcccctggaccagctgcagaactctctggaaact ggcaactgcaccaattactt c/t tccggagacacattcacttggacctccattctcaagctccc ctgctgaagaattttacacgcgcacgttaagtcacgttaagtgagggttgccCTGTATTAGGGGCGCAGG CCA
SLC6A4_u7	SLC6A4	C	A	-	-	noncoding	GE1027	AGCATCAGTAA CCTGCACACTC	ATTTCGAAGCC CGACTGGT	AGCATCAGTAACTGCACACTCTctctctcttaggtctctctggaggaagcg c/a gaccttgccttgccctctattgcagaataacaggggcttaagggACCACTGGCGCTTGCNAAT ctaggtagcagcagggaagtttaaggACCACTGGCGCTTGCNAAT
SLC6A4_u8	SLC6A4	A	G	T	A	cds	GE1079	CTTAGACCCCT GATCTTGA	TCAAGCAAG CAACTCAG	CTTAGACCCCTGATCTTGAactgtctcaggcgccctctgggttttctccctccagagatgccct gggt a g ccagcgttggaactgcagtagctctctgttctggattgtctacttctccagtg ctcggttacatggctggatgaggaatgagatgtgctgtggctggcgcaagacgcacgtaggac ctcggtttctatgcaggtcccttgcctctcactGACGTCTTGTGCTTGA
TBXAS1_1	TBXAS1	C	A	L	I	cds	GE282	CCTTCATCTGC AGCCATT	TGTGACGAA TATGGACGTT A	CTTCATCTGCAGCCATTtaggtgtactcccgacatggctccctacttaccactttgtttatcca tctacagatggctccctctacacgaacgcgcgcctt c/a tctcgcttactttaaagc tatcggaattctggggacgcatttgacatccagagatgaaggtcgtcgtatcacagatgagaatc

FIG. 5IIIIII

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/ noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
TBXAS1 1a16	TBXAS 1	A	G	-	-	noncoding	GE312	CGAGATTGAAA TTTAAAGGAAA GAC	CCAGAAACACA AGTGGTAACTG A	CGAGATTGAAATTTAAGGAAACAGACAAaattgctgagatttgaggtctaaacga[g/c]ctctctc cctttgcagaccctccatcagatggccctgagttctcgagcttcaggaagagcctggccctc cttgacatggtgattgcagagacgtgagatgatacccgagcttccaggtgtggtgtagcc cctccctgcccaggtcccaactcctacccctaccctgcccagctgcagggcagggccct cctccatcAGTTACCACTTGTGTTCGG
TBXAS1 1a17	TBXAS 1	C	T	-	-	noncoding	GE312	CGAGATTGAAA TTTAAAGGAAA GAC	CCAGAAACACA AGTGGTAACTG A	CGAGATTGAAATTTAAGGAAACAGACAAaattgctgagatttgaggtctaaacgaacacattctcctt tgcagaccctccat[c/t]agatggccctgagttctgcagcttcaggaagcctggccctc cttgacatggtgattgcagagacgtgagatgatacccgagcttccaggtgtggtgtagcc cctccctgcccaggtcccaactcctacccctaccctgcccagctgcagggcagggccct cctccatcAGTTACCACTTGTGTTCGG
TBXAS1 1d12	TBXAS 1	C	G	Q	E	cds	GE257	TGCTGTTCCTCA ATTGTTTACTG A	TTCAACACCTG AAATCAAAAT	TGCTGTTCCTCAATTTGTTTACTCAaataagtttgaataatttggaatttttgccttaattcttcttac tatagctggttctcttcaggggtttttggaaagc[c/g]aaatggagctcagaagcgtata tggacctggttgggtaagaagaagaaactcaacggtctctattatgtacgatatcttctattatgt acgatATTTTGATTTTTCAGCTGTGGA
TBXAS1 1d13	TBXAS 1	G	A	R	H	cds	GE316	TGGAACCTAT TCTTTTGCTT T	TACAGGCTAT GCCACTGT	TGGAACCTATTTTTCCTTTTacttcagagagctcagtaattcttaggttctcttaataagagcct aaagctgagtcgaacttcattctcagcttttgaattctgctttctctccaggtcactccacat cagcattctcaagactggagaagtttagcctcagacatcccaagctctctcttcattcattggaac ttgacatttttc[g/a]ccaggttaagggtgcttccattggcttcattcaataataattgctga gggcagggcACAGTGTCTCATGGCTGA
TBXAS1 1d14	TBXAS 1	G	A	-	-	noncoding	GE355	CTTGGAGCATC CTTGTCTCA	GCCTCACCCA GAGAACTGG	CTTGGAGCATCTTGTCTCagatgcagggggtggctcagctggagacagggctgcagaggggaagg gagcgggtgtctgggcccagcctgaccacagacgtcaggtttcacggctgagcccgccgagc agcagggccttcacgtacctcctctggggccgcccacacagagctgctctggggtgcatctta gggtgcttgaggtcaagtgcacactgctccagctgctcacaagttccgggtcccaagctgccc tgagaccaggttgagggccctgctcagagggcag[g/a]tacagggggcagcgggtgggagggcca cccAGTTCTTCTGCTGAGAGC
TBXAS1 1d15	TBXAS 1	G	C	V	L	cds	GE355	CTTGGAGCATC CTTGTCTCA	GCCTCACCCA GAGAACTGG	CTTGGAGCATCTTGTCTCagatgcagggggtggctcagctggagacagggctgcagaggggaagg gagcgggtgtctgggcccagcctgaccacagacgtcaggtttcacggctgagcccgccgagc agcagggccttcacgtacctcctctggggccgcccacacagagctgctctggggtgcatctta gggtgcttgaggtcaagtgcacactgctccac[g/c]tgctgacaaagtccgggtcccaagcct gacctgagaccaggtgagggccctgctcagagggcaggtacagggggcagcgggtgggagggcca cccAGTTCTTCTGCTGAGAGC
TBXAS1 1d16	TBXAS 1	A	C	-	-	noncoding	GE249	ATGGACCTGTA TTGCCACCA	GAGAGTTTCCA TTTCTCATGTC TTA	ATGGACCTGTATTGTCACCAaggtgggttttggcttccctgagctcagacctctgctgtt[a/c] cttcccaacagcgttcgggtttggagttcaagtcggttagccacagcgttctgtttttacgtgac aaaagatgggaagaggtcagaggtgctgctgctgtcttccagctcctgaaagctgaacgaggt AAGACATGAGAAATGCAACTCTC
TBXAS1 1d17	TBXAS 1	C	T	T	M	cds	GE355	CTTGGAGCATC CTTGTCTCA	GCCTCACCCA GAGAACTGG	CTTGGAGCATCTTGTCTCAGatgcagggggtggctcagctggagacagggctgcagaggggaagg gagcgggtgtctgggcccagcctgaccacagacgtcaggtttcacggctgagcccgccgagc agcagggccttc[a/c]tgacctcctctggggccgcccacacagagctgctctggggtgcatctta tctagggctgcttaggttcaagttgacactgctccagctgctcacaagttccaggttcccaagcct gacctgagaccaggtgagggccctgctcagagggcaggtacagggggcagcgggtgggagggcca cccAGTTCTTCTGCTGAGAGC

FIG. 5JJJJJJ

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Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence	
TBXAS1 u2	TBXAS1	G	A	A	T	cds	GE274	CGACCTGGTGT TTCCCTCA	TGCTGCCTCCA CTGGTAAAT	CGACCTGGTGTTCCTCCTCAGattccacgggagggcagctcagagctgcgaggtgctggggcagcg catcccgaggc(g/a)ctgctgtagatggcggtgctgcctgcacatgacctgagcac tggccaaagcccgagagaccttcaacctgaaggtagtactgccccctttaaagctctgaagg gatgtgagtggtgggataagaaTTTACCACTGGAGGCAACA	237
TBXAS1 u3	TBXAS1	C	T	A	A	cds	GE274	CGACCTGGTGT TTCCCTCA	TGCTGCCTCCA CTGGTAAAT	CGACCTGGTGTTCCTCCTCAGattccacgggagggcagctcagagctgcgaggtgctggggcagcg catcccgaggcgctgctagagatggc(g/a)tggtggtgctgcctgcacatgacctgagcac tggccaaagcccgagagaccttcaacctgaaggtagtactgccccctttaaagctctgaagg gatgtgagtggtgggataagaaTTTACCACTGGAGGCAACA	237
TBXAS1 u4	TBXAS1	C	G	Q	E	cds	GE274	CGACCTGGTGT TTCCCTCA	TGCTGCCTCCA CTGGTAAAT	CGACCTGGTGTTCCTCCTCAGattccacgggagggcagctc(g/a)aggactgcaggtgctggggc agcgcatcccgaggcgctgctagagatggc(g/a)tggtggtgctgcctgcacatgacctgagcac tggccaaagcccgagagaccttcaacctgaaggtagtactgccccctttaaagctctgaagg gatgtgagtggtgggataagaaTTTACCACTGGAGGCAACA	237
TBXAS1 u5	TBXAS1	G	A	R	Q	cds	GE355	CTTGGAGCATC CTTGCTCA	GCTCTCACGCA GAGNACTGG	CTTGGAGCATCTTGTCTCAGatgcaggggtggctcagctggagacacagggctgcagagggaggg gagcgggtgcttggggcagccctgaccacacagggagctcaggttcacggctgagggccggcagc agcagggcccttcacgtacctgctggccttggggccgcccacagggagctgctgcctgagcatca ggctgcttggagtcaggtgacactgctccagctgctcacaagtcc(g/a)gttccagacct ggcctgagaccaggtgagggccctgctcagaggcaggtacagggggcagcggtgggagggcca CCCCAGTTCCTCGGTGAGAGC	347
TBXAS1 u6	TBXAS1	T	G	V	G	cds	GE470	GGCCCTGGTTT ATTATCAC	CCAAAGTGGCC TCCATTTC	GGCCCTGGTTTATTATATCACCCctcttcaatgccactttgtttctcttccaagtatcatttc catccataatggtcccactggccggatgttggcccaataagaaacagagagactgaatggcttt tttaacaactcattaggaatg(lt/g)gattgcttggggccagcaagctgccgaagaggttaa cgatatttaattagggacacagcttgaatgGAATGGAGCCGCACTTTGG	243
TBXAS1 u7	TBXAS1	T	C	I	T	cds	GE912	GGCCATGTATC TTCCCTCTTT	GGGGATCCAA CTTGTACT	GGCCATGTATCTTCTCTCTTTgttctccaggagggcctcactctctatgactgaaggtcaaaaatg tgcaattttctctctttgttctcttagaggcggagagacttctccaaaatggctctggatgccga catctgcaagtcctcatggcgtagagactttgacatgtagagagctttctctctactgg gtgcaagccgaaccttccggcaacacacagccagccctatggccagggctttgactgtggaag aga(lt/c)gtggggcagggcttcatctctctcatgctggtgctggaatcatcaccaacact ttctttgcccacttactggtgcccacacccctgactgctgccaagagaagcttctgagagaggtag acgttttttaaggagaaacacgtgAGTACAGTTGGATCCCTCC	432
TBXAS1 u8	TBXAS1	C	G	L	V	cds	GE912	GGCCATGTATC TTCCCTCTTT	GGGGATCCAA CTTGTACT	GGCCATGTATCTTCTCTCTTTgttctccaggagggcctcactctctatgactgaaggtcaaaaatg tgcaattttctctctttgttctcttagaggcggagagacttctccaaaatggctctggatgccga catctgcaagtcctcatggcgtagagactttgacatgtagagagctttctctctactgg gtgcaagccgaaccttccggcaacacacagccagccctatggccagggctttgactgtggaag agattgtggggcagggcttcatctctctcatgctggtgctggaatcatcaccaacacttct tttggccacctac(lt/g)actggccacacacccctgactgctgccaagagaagcttctgagagaggtag acgttttttaaggagaaacacgtgAGTACAGTTGGATCCCTCC	432
TBXAS1 u9	TBXAS1	T	G	M	R	cds	GE274	CGACCTGGTGT TTCCCTCA	TGCTGCCTCCA CTGGTAAAT	CGACCTGGTGTTCCTCCTCAGattccacgggagggcagctcagagctgcgaggtgctggggcagcg catcccgaggcgctgctagaga(lt/g)ggccgtgggtgctgcctgcacatgacctgagcac tggccaaagcccgagagaccttcaacctgaaggtagtactgccccctttaaagctctgaagg gatgtgagtggtgggataagaaTTTACCACTGGAGGCAACA	237

FIG. 5KKKKKKK

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Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' → 3')	Reverse Primer (5' → 3')	Assay Sequence
THBDu1	THBD	T	G	C	G	cds	GE409	TCGGCTTACAG CTAATGTGC	GCCAGCTAAGG TCCTTTGCT	TCGGCTTACAGCTAATGTGCACCGCGCCCGGAGCGGTCCAGGGGCACTGGGCCAGGAGGCG CCGGGCGCTTGGGACTGCGAGTGGAGAACGCGGCTCGGACGCTGCGATCGATCCCTGG GGCTCCCGCTGCCAGTGCACCGCGCGCCCTCGAGGACGAGACGGGCGCTCTGCCACCAT CCGAGCGAGTCTCTCAAGCACTCTCGAGCACTCTTCGTTCCCAACCCCGCCAGCCGCGGC TCTACTCTGTGATGTGGAGACCGGTACCGGTGGCGCCGACCAACACCGGTGCGAGGACGT GGATGACTCATCTGGAGCCCGTCTCGCGAGCTGTCTCAACACAGAGGTGGTCTCG AGTGCCTGCTACCTAAGTCTGGTGGAGCGGAGT/GJGTGGAGCGGTGGACCC ATGCTCAGAGCAACTCGAGTACCACTGCCAGCCCTGAACCAACTGACTCTGGCTCT GCGCGGGGCTTCGCCCCATCCCAACGCGCGCAAGGTGCCAGATTTTGAACCAAGAT GCTTCAGCGGACTGCAACCAACCAAGGTAGTGTGAGTCCCTGAAGGTACATCTCT GGACGCGGTTTCTCTGCAAGGACATCGAGAGTTCGAACACGCGGCTCTCTCGGAGTGT GCCACAACCTCCCGGTACCTTGAAGTGCATCTGGGCGCGCACTGGCCCTTGCCTCGCACTT GGACCGAGTGTGCTCCGCGAGGTGGAGTGGCGAGCGGTCTGGCGAGCCCGCCCGAG CCCGAGCCCGGCTCCACTTGACTCTCCCGCGTGGGCTGTGATTCGGGCTTGTCTCATAG GCATCTCATCGCGAGCTGTGCTGGTGGTCTTTGGGCTCTCTGCGCTCTCTGCCACTGCGCAAG AAGCAGGGCGCGCCAGGCGCAAGATGGAGTACAAAGTGGCGGCGCCCTT
THBDu2	THBD	C	A	P	T	cds	GE409	TCGGCTTACAG CTAATGTGC	GCCAGCTAAGG TCCTTTGCT	TCGGCTTACAGCTAATGTGCACCGCGCCCGGAGCGGTCCAGGGGCACTGGGCCAGGAGGCG CCGGGCGCTTGGGACTGCGAGTGGAGAACGCGGCTCGGACGCGTGCATGCGATCCCTGG GGCTCCCGCTGCCAGTGCACCGCGCGCCCTCGAGGACGAGACGGGCGCTCTGCCACCAT CCGAGCGAGTCTCTCAAGCACTCTCGAGCACTCTTCGTTCCCAACCCCGCCAGCCGCGGC TCTACTCTGTGATGTGGAGACCGGTACCGGTGGCGCCGACCAACACCGGTGCGAGGACGT GGATGACTCATCTGGAGCCCGTCTCGTCTCGCGAGCGGTGTCAACACAGAGGTGGTCTCG AGTGCCTGCTACCTAAGTCTGGTGGAGCGGAGTGTGGAGCCGTGGACCCGTGCT TTCAGAGCAACTGCGAGTACCACTGCGCAG C/A CCCTGAACCAACTGACTCTCTGCTCT GCGCGAGGGCTTCGCCCCATCCCAACGCGCGCAAGGTGGAGCGGTCTGGCGAGCCCGCCCGAG GCCTTCCAGCCGACTGCAACCAACCCAGGTAGTGTGAGTCCCTGAAGGTACATCTCT GGACGCGGTTTCTCTGCAAGGACATCGAGAGTTCGAACACGCGGCTCTCTCGGAGTGT GCCACAACCTCCCGGTACCTTGAAGTGCATCTGGGCGCGCACTGGCCCTTGCCTCGCACTT GGACCGAGTGTGCTCCGCGAGGTGGAGTGGCGAGCGGTCTGGCGAGCCCGCCCGAG CCCGAGCCCGGCTCCACTTGACTCTCCCGCGTGGGCTGTGATTCGGGCTTGTCTCATAG GCATCTCATCGCGAGCTGTGCTGGTGGTCTTTGGGCTCTCTGCGCTCTCTGCCACTGCGCAAG AAGCAGGGCGCGCCAGGCGCAAGATGGAGTACAAAGTGGCGGCGCCCTT

FIG. 5L11111111

Poly Id	Gene	ref NT	alt NT	ref AA	alt AA	coding/noncoding	Assay #	Forward Primer (5' -> 3')	Reverse Primer (5' -> 3')	Assay Sequence
THP0d5	THPO	C	?	-	-	noncoding	GE345	TCACTCTGCTG GCTACTCTCTAA	CCTTCTTCCT CAGGTCCTCTA	TCACCTGCTGCTACTCTTAAggtccccaccgccttttagtggccctttgagcgagtgcgct 336 ctctcttccatctcttctcagagagagaccagagacattctggagcagtgacccctt ctgtggaggagtgatggcagcagcgaggaacactggaccacttgcctctcctcctctggg gcagcttcttgaaaggtccgtctctctcttggggccctgcagagccctcttggaacccaggtaa gtccccagtcagggtctgtagaacctgtcttcttctgactcagtcctc/ctAGAAGACCTG AGGAAGAGG
THP0u1	THPO	T	A	S	T	cds	GE416	GGCATCTCTGTC TTTCTCTACTTA GAC	AGGAATCTTG TCCAGTTGTCT C	GGCATCTCTGTCCTTACTTAAgaggggctcagatctggccctgggttttggccctcagg 844 accatctctgcctcagcttctctccagagggagggaccagctcacaggtatcccaatgccat cttctcagcttcccaacacctgctccagagaaagtgcttctctgatctctgtagaggtcca ccctcagctcagggggcccccaccaccagctgtccccagacgaacctctagtcctca ctgaacgagctcccaacacaggaactctggatgttggagacaaacttactgctt/a/cagcca gaactactggctctgggtctctgaagtggcagggattcagagcccaagattctgtgctgtg aaccaacctccaggtccctggaccacaaatccccggaacctgaacaggaatcacgaactctgaa tggaaactcgtggaactcttcttggaacctcacgcaggaacctaggagcccggaatttctcag gaacacagacacaggtctctgcacccaacctccagctggatattctcttccccaaacct ccctcactggagagatacgtctctctctctctccaccaaccttgccacctgtgtctcagct ccacccctgtctctgacctctgtctccacgccccaccctaccagcccttcttaacacat cctacacccactcccaaatctgtctcaggaaggttaaggttctcagacactgccgacatcagca ttgtctcgtgtacagctcccttctcctcaggggccccctggGAGACACTGACAGATTTCTT TGAGGACTAGCTCTCTTATTAGgtaccatagctctctctatttcagctcccttctccccac 244 caatcttttcaacagagcc(a/g)gtgccagaggttcaaccttgcctacacctgtctctgtg cctcgtgtggactttagcttgggagatgaaacacccagatgtaagaagccatcccttaacct gggtctcccaagctcgtctctcagttctccACTCTTCCCATGGATTC
THP0u2	THPO	A	G	Q	R	cds	GE265	TGGAGGACTAG CCTGCTTATTA	AGAAATCCATGG GAAGCAGTG	GGCATCTCTGTCCTTACTTAAgaggggctcagatctggccctgggttttggccctcagg 844 accatctctgcctcagcttctctccagagggagggaccagctcacaggtatcccaatgccat cttctcagcttcccaacctgctccagagaaagtgcttctctgatgtctgtagaggtcca ccctcagctcagggggcccccaccaccagctgtccccagacgaacctctagtcctca ctgaacgagctcccaacacaggaactctggatgttggagacaaacttactgctcctcaggaac tactggctctgggtctctgaagtggcagcag(g/a)gattcagagccaaagtctctgtgctgtg aaccaacctccaggtcccttgaccacaaatccccggaacctgaacaggaatcacgaactctgaa tggaaactcgtggaactcttcttggaacctcacgcaggaacctaggagcccggaatttctcag gaacacagacacaggtctctgcacccaacctccagctggatattctcttccccaaacct ccctcactggagagatacgtctctctcttccaccaaccttgccacctgtgtctcagct ccacccctgttctcagccctctgtctccacgccccaccctaccagcccttcttaacacat ccttaacccactcccaaatctgtctcaggaaggttaaggttctcagacactgccgacatcagca ttgtctcgtgtacagctcccttctcctcaggggccccctggGAGACACTGACAGATTTCTT
THP0u3	THPO	G	A	G	R	cds	GE416	GGCATCTCTGTC TTTCTCTACTTA GAC	AGGAATCTTG TCCAGTTGTCT C	GGCATCTCTGTCCTTACTTAAgaggggctcagatctggccctgggttttggccctcagg 844 accatctctgcctcagcttctctccagagggagggaccagctcacaggtatcccaatgccat cttctcagcttcccaacctgctccagagaaagtgcttctctgatgtctgtagaggtcca ccctcagctcagggggcccccaccaccagctgtccccagacgaacctctagtcctca ctgaacgagctcccaacacaggaactctggatgttggagacaaacttactgctcctcaggaac tactggctctgggtctctgaagtggcagcag(g/a)gattcagagccaaagtctctgtgctgtg aaccaacctccaggtcccttgaccacaaatccccggaacctgaacaggaatcacgaactctgaa tggaaactcgtggaactcttcttggaacctcacgcaggaacctaggagcccggaatttctcag gaacacagacacaggtctctgcacccaacctccagctggatattctcttccccaaacct ccctcactggagagatacgtctctctcttccaccaaccttgccacctgtgtctcagct ccacccctgttctcagccctctgtctccacgccccaccctaccagcccttcttaacacat ccttaacccactcccaaatctgtctcaggaaggttaaggttctcagacactgccgacatcagca ttgtctcgtgtacagctcccttctcctcaggggccccctggGAGACACTGACAGATTTCTT

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FIG. 5NNNNNNN

[illegible]

FIG. 500000000

[illegible]

FIG. 5Q QQQQQQ

(19) World Intellectual Property Organization
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SKLAR, Pamela [US/US]; 68 Fuller Street, Brookline, MA 02446 (US).

(21) International Application Number: PCT/US00/08440

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(74) Agents: HOGLE, Doreen, M. et al.; Hamilton, Brook, Smith & Reynolds, P.C., Two Militia Drive, Lexington, MA 02421 (US).

(25) Filing Language: English

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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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Published:

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(88) Date of publication of the international search report:
23 August 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: CHARACTERIZATION OF SINGLE NUCLEOTIDE POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES

(57) Abstract: The invention provides nucleic acid segments of the human genome, particularly nucleic acid segments from the coding region of a gene, including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking or containing these sites are also provided. The nucleic acids, primers and probes are used in applications such as phenotype correlations, forensics, paternity testing, medicine and genetic analysis.

WO 00/58519 A3



INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 00/08440

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 96 20279 A (RIBOZYME PHARM INC ;WARNER LAMBERT CO (US)) 4 July 1996 (1996-07-04) p. 15, sequence "013a" ---	1
X	US 5 705 388 A (COUTURE L. ET AL.) 6 January 1998 (1998-01-06) SEQ ID 622,623 --- -/--	1

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

10 November 2000

Date of mailing of the international search report

22.02.01

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Luzzatto, E

INTERNATIONAL SEARCH REPORT

Interr 1al Application No
PCT/US 00/08440

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE MEDLINE [Online] American medical association Accession Number 92172843, 3 March 1992 (1992-03-03) XP002152537 abstract & SUMI-ICHINOSE C. ET AL.: "Molecular cloning of genomic DNA and chromosomal assignment of the gene for human aromatic L-amino acid decarboxylase, the enzyme for catecholamine and serotonin biosynthesis" BIOCHEMISTRY, vol. 31, no. 8, 1992, pages 2229-2238, US</p>	1,11
A	<p>--- CHEE M ET AL: "ACCESSING GENETIC INFORMATION WITH HIGH-DENSITY DNA ARRAYS" SCIENCE,US,AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, vol. 274, 25 October 1996 (1996-10-25), pages 610-614, XP002022508 ISSN: 0036-8075 cited in the application the whole document</p>	1-12
A	<p>--- WANG D G ET AL: "Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome" SCIENCE,US,AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, vol. 280, 1998, pages 1077-1082, XP002089398 ISSN: 0036-8075 cited in the application the whole document</p>	1-12
A	<p>--- OEFNER P J ET AL: "COMPARATIVE DNA SEQUENCING BY DENATURING HIGH-PERFORMANCE LIQUID CHROMATOGRAPHY" AMERICAN JOURNAL OF HUMAN GENETICS,UNIVERSITY OF CHICAGO PRESS, CHICAGO,,US, vol. 57, October 1995 (1995-10), page A266 XP002918646 ISSN: 0002-9297 cited in the application the whole document</p>	1-12
A	<p>--- WO 98 20165 A (WHITEHEAD BIOMEDICAL INST ;HUDSON THOMAS (US); LANDER ERIC S (US);) 14 May 1998 (1998-05-14) page 4, line 1 -page 27, line 23 ---</p>	1-12
	-/--	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/08440

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE GENE BANK [Online] accession number M84597, 18 April 1992 (1992-04-18) ICHINOSE H. ET AL.: "Molecular cloning of genomic DNA and chromosomal assignment of the gene for human aromatic L-amino acid decarboxylase" XP002152538 abstract</p>	
A	<p>--- SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS, USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, US, UNIVERSITY OF CHICAGO PRESS, CHICAGO,, vol. 52, no. 1, 1993, pages 46-59, XP002050638 ISSN: 0002-9297 the whole document</p>	11,12
A	<p>--- UNDERHILL P.A. ET AL.: "Detection of numerous Y chromosome biallelic polymorphisms by denaturing high-performance liquid chromatography" GENOME RESEARCH, vol. 7, - 1997 pages 996-1005, XP000942730 US abstract</p> <p>-----</p>	1-12

INTERNATIONAL SEARCH REPORT

In. ational application No.
PCT/US 00/08440

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-12 all partly

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-12 (all partly)

Nucleic acid molecules comprising the polymorphic sites present in the sequences SEQ ID 1927 and 1928 given on fig. 5A (which correspond to the sequences designated AADCd4 and AADCd5 in fig. 5A), and methods based thereon.

2. Claims: 1-12 (all partly)

Nucleic acid molecules comprising the polymorphic site(s) present in each of the sequences given on figs. 5A (except the sequences AADCd4 and AADCd5), 5B-5QQQQQQ and methods based thereon.

The sequences differing only at one or more polymorphic sites are considered to belong to the same invention. The different inventions are summarised as indicated in the following table (see annex), where col. 1 and 3 show the SEQ ID number and col. 2 and 4 the length of the sequence. The total number of inventions is 396.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/08440

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9620279	A	04-07-1996	US 5705388 A	06-01-1998
			AU 4419596 A	19-07-1996
			CA 2208502 A	04-07-1996
			EP 0800580 A	15-10-1997
			JP 10511269 T	04-11-1998
US 5705388	A	06-01-1998	AU 4419596 A	19-07-1996
			CA 2208502 A	04-07-1996
			EP 0800580 A	15-10-1997
			JP 10511269 T	04-11-1998
			WO 9620279 A	04-07-1996
WO 9820165	A	14-05-1998	EP 0941366 A	15-09-1999